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From: Kemmerer, Elizabeth
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Please search SEQ ID NO: 2 for 10/004832.

Thanks,

Elizabeth (Betsy) Kemmerer
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TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
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OM protein - protein search, using sw model

Run on: September 23, 2003, 14:58:07 ; Search time 87 Seconds
(without alignments)
259.071 Million cell updates/sec

Title: US-10-004-832-2

Perfect score: 735
Sequence: 1 MDSLVCEVPELLEKLRK.....IRTDLLEAWLQKLSFPR 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_19Jun03:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	735	100.0	142	16	HAAR81309
2	735	100.0	142	20	AAV39813
3	735	100.0	142	21	AAAB21089
4	735	100.0	142	21	AAV54900
5	735	100.0	142	23	AAE14612
6	735	100.0	142	24	ABG74162
7	699	95.1	147	21	AAAB58304
8	616	83.8	155	14	AAAR43941
9	570	77.6	178	22	ABG19927

10	558	75.9	109	20	AAV36208
11	513.5	69.9	126	22	ABG19926
12	464.5	63.2	116	21	AAAG03953
13	376	51.2	141	22	ABAB61879
14	247.5	33.7	58	22	ABG19924
15	167	22.7	46	22	ABG19925
16	154	21.0	113	24	ABR41794
17	148	20.1	27	14	AAAR43949
18	113	15.4	350	16	AAAR76598
19	113	15.4	350	23	ABG96404
20	113	15.4	385	21	AAAB53426
21	113	15.4	385	22	AAAG73824
22	111.5	15.2	133	21	AAAG05223
23	111.5	15.2	133	21	AAAG37448
24	111.5	15.2	133	21	AAAG41989
25	111.5	15.2	140	21	AAAG05222
26	111.5	15.2	140	21	AAAG41988
27	111.5	15.2	170	21	AAAG41987
28	109.5	14.9	343	22	ABAB5681
29	109	14.8	349	22	AAW78942
30	109	14.8	349	22	AAAB5617
31	109	14.8	351	20	AAV22216
32	109	14.8	399	22	AAW79926
33	108	14.7	132	21	AAAG04373
34	108	14.7	132	21	AAAG05741
35	108	14.7	132	21	AAAG10071
36	108	14.7	139	21	AAAG05740
37	108	14.7	139	21	AAAG10070
38	108	14.7	150	21	AAAG04372
39	108	14.7	348	22	AAU09098
40	105	14.3	132	21	AAAG11685
41	105	14.3	132	21	AAAG47845
42	105	14.3	139	21	AAAG11684
43	105	14.3	178	21	AAAG47844
44	104	14.1	132	21	AAAG15710
45	104	14.1	132	21	AAAG47863

ALIGNMENTS

RESULT 1
ID AAR81309 strand: Protein; 142 AA.
XX AAR81309;
AC AAR81309;
XX 22-DEC-1995 (first entry)
DT 22-DEC-1995 (first entry)
XX
DE Haematopoietic maturation factor.
XX
KW Haematopoietic maturation factor; cancer; leukemia; hemophilia.
XX
OS Homo sapiens.
XX
PN W09519985-A1.
XX
PD 27-JUL-1995.
XX
XX 10-MAY-1994; 94WO-US05186.
XX
XX 25-JAN-1994; 94US-0187186.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Adams MD, Kirkness E, Olsen H, Rosen C;
XX WPI: 1995-269411/35.
XX N-PSDB: AAG09843.
XX
XX New DNA encoding human haematopoietic maturation factor - useful in
XX treatment and diagnosis, e.g. of cancer, leukaemia, haemophilia etc.
XX

PS Claim 9; Fig.1; 44pp; English.

CC New cDNA (ATCC 75514) encoding human hematopoietic maturation factor is
isolated from cDNA libraries derived from early stage kidney, spleen,
CC thymus or leukocytes and amplified using primers corresp. to the 5'
CC and 3' end of the gene. Recombinant protein is obt'd. by expression
CC of the cDNA in host cells.

XX Sequence 142 AA;

SO Query Match 100.0%; Score 735; DB 16; Length 142;

Best Local Similarity 100.0%; Pred. No. 6.7e-74;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDSLVCEVDPPELTETLRKFRFRKETDAAIIMKVDKROMVYLEEFONISPEELKME 60
Db 1 MSDSLVCEVDPPELTETLRKFRFRKETDAAIIMKVDKROMVYLEEFONISPEELKME 60
QY 61 LPERQPRFVVSYYKVVHDDGRVSYPLCFIFSSPGCKPEQOMYAGSKNRLVQTAEITKV 120
Db 61 LPERQPRFVVSYYKVVHDDGRVSYPLCFIFSSPGCKPEQOMYAGSKNRLVQTAEITKV 120
QY 121 FEIRTTDLTAMLOEKLSFRR 142
Db 121 FEIRTTDLTAMLOEKLSFRR 142

RESULT 2

AA39813
ID AAY39813 standard; Protein; 142 AA.

XX AAY39813;

DT 02-DEC-1999 (first entry)

XX CBFBOE11 protein sequence.

XX CBFBOE11; glia maturation factor beta; vaccine; cancer; therapy;

KW neurological disease; autoimmune disease.

XX Homo sapiens.

OS WO9946291-A1.

PN 16-SEP-1999.

PD 12-MAR-1998; 98WO-CN00033.

XX 12-MAR-1998; 98WO-CN00033.

PA (UYSH-) UNIV SHANGHAI SECOND MEDICAL.

PI Fu G, Shen Y, Mao M, Wang Y;

DR WPI; 1999-561662/47.

XX N-PSDB; AA220679.

PT New polynucleotide encoding a glia maturation factor homologue, useful
for treating cancer, neurological disease and autoimmune disease -

XX Claim 11; Page 22; 29pp; English.

XX This sequence represents the human CBFBOE11 protein of the invention.

CC CBFBOE11 is homologous to glia maturation factor beta. The CBFBOE11
coding sequence, vectors containing it and recombinant host cells are
useful for recombinant production of CBFBOE11. The CBFBOE11 DNA, protein,
CC and antibodies against CBFBOE11 are useful as research reagents, for
screening assays and in diagnostic assays. Antagonists and agonists of
CC CBFBOE11 can be used to inhibit or enhance, respectively, the activity of
CC CBFBOE11 or expression of the DNA. Anti-CBFBOE11 antibodies and CBFBOE11
or its fragments can be used in vaccines. In particular, the proteins,
CC antibodies, agonists and antagonists can be used for treating,
CC e.g. cancer and neurological disease and autoimmune disease, related to

CC both an excess and insufficient amounts of CBFBOE11.

XX Sequence 142 AA;

SO Query Match 100.0%; Score 735; DB 20; Length 142;
Best Local Similarity 100.0%; Pred. No. 6.7e-74;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDSLVCEVDPPELTETLRKFRFRKETDAAIIMKVDKROMVYLEEFONISPEELKME 60
Db 1 MSDSLVCEVDPPELTETLRKFRFRKETDAAIIMKVDKROMVYLEEFONISPEELKME 60
QY 61 LPERQPRFVVSYYKVVHDDGRVSYPLCFIFSSPGCKPEQOMYAGSKNRLVQTAEITKV 120
Db 61 LPERQPRFVVSYYKVVHDDGRVSYPLCFIFSSPGCKPEQOMYAGSKNRLVQTAEITKV 120
QY 121 FEIRTTDLTAMLOEKLSFRR 142
Db 121 FEIRTTDLTAMLOEKLSFRR 142

RESULT 3

AAB21089
ID AAB21089 standard; Protein; 142 AA.

XX AAB21089;

DT 19-DEC-2000 (first entry)

DE Human CBFBOE11 protein, a neuroglia mature factor beta homologue.

XX Human CBFBOE11; neuroglia mature factor beta homologue;

KW GMF-beta homologue; cancer; neurological disease; autoimmune disease.

XX Homo sapiens.

PN CN125927-A.

PD 07-JUN-2000.

PF 12-MAR-1998; 98CN-0805074.

XX 12-MAR-1998; 98CN-0805074.

PA (UYSH-) UNIV SHANGHAI NO 2 MEDICAL.

PI Fu G, Shen Y, Mao Y;

DR WPI; 2000-525018/48.

XX N-PSDB; AAA90298.

PT Human neuroglia mature factor (GMF) beta homologous gene (CBFBOE11) -

XX Claim 1; Page 12; 25pp; Chinese.

XX This sequence represents human CBFBOE11 protein. CBFBOE11 is a
homologue of neuroglia mature factor beta (GMF-beta). The invention
CC also encompasses the recombinant production of CBFBOE11 protein. The
invention additionally relates to methods of utilizing CBFBOE11 proteins
CC and nucleotides in the design of protocols for the treatment of disorders
CC such as cancer, neurological disease, and autoimmune disease. The
CC CBFBOE11 proteins and nucleotides may also be used in the diagnosis
of such conditions.

XX Sequence 142 AA;

SO Query Match 100.0%; Score 735; DB 21; Length 142;
Best Local Similarity 100.0%; Pred. No. 6.7e-74;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDSLVCEVDPPELTETLRKFRFRKETDAAIIMKVDKROMVYLEEFONISPEELKME 60
Db 1 MSDSLVCEVDPPELTETLRKFRFRKETDAAIIMKVDKROMVYLEEFONISPEELKME 60

QY 61 LPEROPREVVYXSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120
 |||||||
 DB 61 LPEROPREVVYXSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120
 |||||||
 QY 121 FEIRTTDDLTEAMLOEKLSPFR 142
 |||||||
 DB 121 FEIRTTDDLTEAMLOEKLSPFR 142
 |||||||

RESULT 4
 AAY54900
 ID AAY54900 standard; Protein; 142 AA.
 XX AAY54900;
 AC
 XX 09-FEB-2000 (first entry)
 DT
 XX Human haemopoietic maturation factor protein sequence.
 DE
 XX Haemopoietic maturation factor; HMF; human; HMF; leukaemia; haemolysis;
 KW cell proliferation inhibitor; T-cell proliferation; polycythemia vera;
 KW lymphocyte proliferation; haematopoietic progenitor cell formation;
 KW blood disorder; myelodysplasia; haemophilia; splenomegaly; therapy.
 XX
 OS Homo sapiens.
 XX
 PN US586669-A.
 XX
 PD 16-NOV-1999.
 XX
 PF 16-MAY-1995; 95US-0442497.
 XX
 PR 25-JAN-1994; 94US-0187186.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Olsen HS, Rosen CA, Kirkness EF, Adams MD;
 XX
 DR WPI: 2000-037451/03.
 DR N-PSDB: AA237459.

PT Haemopoietic maturation factor polypeptide useful for inhibiting
 PT leukaemia cell proliferation, stimulating T-cell proliferation and
 PT differentiation, stimulating thymocyte proliferation and stimulating
 PT haemopoietic progenitor cell formation -
 PS
 CC Claim 1; Fig 1; 27pp: English.
 CC
 CC This sequence is the human haemopoietic maturation factor (HMF) of
 CC the invention. The HMF polypeptide is capable of inhibiting leukaemia
 CC cell proliferation, stimulating T-cell proliferation and differentiation,
 CC stimulating thymocyte proliferation and stimulating haematopoietic
 CC progenitor cell formation. HMF is useful for treating leukaemia and other
 CC blood disorders, e.g. haemolysis, polycythemia vera, myelodysplasia,
 CC haemophilia and splenomegaly, and for inducing differentiation of
 CC immature malignant leukaemia cells. HMF has a narrower range of
 CC activities and greater specificity for functionally differentiated cells
 CC than general growth factors and so can be used to treat diseases specific
 CC for the activities it regulates.
 CC
 XX
 XX
 SQ Sequence 142 AA;
 Query Match 100.0%; Score 735; DB 21; Length 142;
 Best Local Similarity 100.0%; Pred. No. 6,7e-74;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDSLVCEVDPPELTKLRFRFRKETDAAIIMKVDKROMVYLEEFQNIISPEELKME 60
 |||||||
 DB 1 MSDSLVCEVDPPELTKLRFRFRKETDAAIIMKVDKROMVYLEEFQNIISPEELKME 60
 |||||||
 QY 61 LPEROPREVVYXSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120
 |||||||

DB 61 LPEROPREVVYXSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120
 |||||||
 QY 121 FEIRTTDDLTEAMLOEKLSPFR 142
 |||||||
 DB 121 FEIRTTDDLTEAMLOEKLSPFR 142
 |||||||

RESULT 5
 AAE14612
 ID AAE14612 standard; Protein; 142 AA.
 XX AAE14612;
 AC
 XX 18-JUN-2002 (first entry)
 DT
 XX Human haemopoietic maturation factor.
 DE
 XX Human; haemopoietic maturation factor; HMF; T cell; graft rejection;
 KW autoimmune disease; leukaemia; blood-related disorder; haemolysis;
 KW haemophilia; splenomegaly; malignant.
 XX
 OS Homo sapiens.
 XX
 PN US6346246-B1.
 XX
 PD 12-FEB-2002.
 XX
 PF 15-JUN-1999; 99US-0333033.
 XX
 PR 16-MAY-1995; 95US-0442497.
 XX
 PR 25-JAN-1994; 94US-0187186.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Kirkness EF, Adams MD, Olsen HS, Rosen CA;
 XX
 DR WPI: 2002-224985/28.
 DR N-PSDB: AAD27921.

PT New antibody that specifically binds to human haematopoietic maturation
 PT factor polypeptide, useful to prevent T cell expansion for treating
 PT graft rejection and autoimmune diseases -
 PS
 CC Claim 1; Fig 1; 24pp: English.
 CC
 CC The invention relates to an antibody that specifically binds to
 CC human haemopoietic maturation factor (HMF). The antibody is useful as an
 CC antagonist of HMF polypeptide, to prevent expansion of T cells which may
 CC be employed for treating conditions related to the presence of T cells
 CC e.g. graft rejection and autoimmune diseases. The antibody
 CC is also useful to isolate HMF polypeptide from tissue expressing the
 CC polypeptide, and in diagnostic assays for detecting altered levels of
 CC the polypeptide in various tissues. The HMF polypeptide and
 CC polynucleotide are useful for therapeutic purposes, e.g. to treat
 CC leukaemia, blood-related disorders (e.g. haemolysis, haemophilia,
 CC splenomegaly), to stimulate differentiation and proliferation of cells of
 CC haematopoietic or stromal origin, and to remove malignant cells.
 CC The present sequence is human haemopoietic maturation factor.
 CC
 XX
 XX
 SQ Sequence 142 AA;
 Query Match 100.0%; Score 735; DB 23; Length 142;
 Best Local Similarity 100.0%; Pred. No. 6,7e-74;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDSLVCEVDPPELTKLRFRFRKETDAAIIMKVDKROMVYLEEFQNIISPEELKME 60
 |||||||
 DB 1 MSDSLVCEVDPPELTKLRFRFRKETDAAIIMKVDKROMVYLEEFQNIISPEELKME 60
 |||||||
 QY 61 LPEROPREVVYXSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120
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 DB 61 LPEROPREVVYXSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120
 |||||||

QY 121 FEIRTTDDLTEAWLQEKLSFFR 142
 DB 121 FEIRTTDDLTEAWLQEKLSFFR 142

RESULT 6
 ABG74162
 ID ABG74162 standard; Protein: 142 AA.

XX ABG74162;

XX 06-MAY-2003 (first entry)

XX Human haemopoietic maturation factor.

XX Human: haemopoietic maturation factor; HMF; haemopoiesis; bone marrow;
 KW stromal cell differentiation; mature blood cell differentiation; HIV;
 KW T cell proliferation; T cell differentiation; gene therapy; leukaemia;
 KW anaemia; thrombocytopenia; granulocytopenia; blood-related disorder;
 KW haemolysis; polycythemia vera; haemophilia; T cell deficiency disease;
 KW immature malignant leukaemia cell differentiation; graft rejection;
 KW haematopoietic cell precursor replacement; bone marrow transplant;
 KW autoimmune disease.

XX Homo sapiens.

XX US2002146408-A1.

XX 10-OCT-2002.

XX 07-DEC-2001; 2001US-0004832.

XX 16-MAY-1995; 95US-0442497.

XX 15-JUN-1999; 99US-0333033.

XX 25-JAN-1994; 94US-0187186.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Kirkness EF, Adams MD, Olsen HS, Rosen CA;

XX WPI; 2003-228012/22.

XX N-PSDB; ABX16160.

XX New isolated hemopoietic maturation factor polypeptide useful for
 PT stimulating hemopoiesis, for treating leukemia, anemia,
 PT thrombocytopenia, and granulocytopenia.

PS Claim 16; Fig 1; 27pp; English.

XX The invention relates to an isolated haemopoietic maturation factor (HMF)
 CC polypeptide encoded by DNA of American Type Culture Collection (ATCC)
 CC Deposit No. 75514, and their fragments, analogues or derivatives. The
 CC polypeptide is useful for treating a patient having a need of HMF. The
 CC polypeptide and a host cell genetically engineered with the polypeptide
 CC are useful for identifying compounds active as agonists or antagonists to
 CC HMF. The nucleic acid encoding the polypeptide is useful for diagnosing a
 CC disease or susceptibility to a disease related to the underexpression of
 CC HMF. A host cell genetically engineered with the nucleic acid is useful
 CC for treating a patient having the need to inhibit HMF. The polypeptide is
 CC used in a diagnostic process by analysing for the presence of the
 CC polypeptide in a sample from a host. The polypeptide is useful for
 CC treating leukaemia, anaemia, thrombocytopenia and granulocytopenia, other
 CC blood-related disorders e.g. haemolysis, polycythemia vera, haemophilia
 CC and diseases caused by T cell deficiencies e.g. leukaemia and human
 CC immunodeficiency virus (HIV) infection. The polypeptide stimulates
 CC differentiation of immature malignant leukaemia cells. The polypeptide
 CC can be used to offset the destruction of haematopoietic cell precursors
 CC which occurs during radiation or chemotherapy by expanding the stromal
 CC cell population and the subsequent expansion of haematopoietic cells and
 CC stimulates the differentiation of mature blood cells in situations where
 CC a patient has undergone a bone marrow transplant. The polypeptide is also
 CC useful for stimulating bone marrow/haematopoietic cells in vitro for gene
 CC therapy purposes, for stimulation of bone marrow recovery due to

CC chemotherapy, for stimulating proliferation and differentiation of
 CC certain human T cell populations. The nucleic acid is useful as a probe
 CC for a cDNA library to isolate other genes which have high sequence
 CC similarity to the HMF gene or other similar biological activity and for
 CC chromosomal identification. A compound which inhibits the polypeptide is
 CC useful for preventing expansion of T cell populations, for treating
 CC conditions such as graft rejection and autoimmune diseases. The present
 CC sequence represents the amino acid sequence of human haemopoietic
 CC maturation factor.

XX Sequence 142 AA;

XX Query Match 100.0%; Score 735; DB 24; Length 142;

XX Best Local Similarity 100.0%; Pred. No. 6,7e-74;

XX Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDSLVCEVDPELTETLRKFRKEDNAAIIMKVKDKRMVYLSEFQISPEELKME 60

DB 1 MSDSLVCEVDPELTETLRKFRKEDNAAIIMKVKDKRMVYLSEFQISPEELKME 60

QY 61 LPERQPRFVYVSYKYVHDGKRVSLPCFIFSSPVGCKPEQOMYAGSKNRLVOTAEILTKV 120

DB 61 LPERQPRFVYVSYKYVHDGKRVSLPCFIFSSPVGCKPEQOMYAGSKNRLVOTAEILTKV 120

QY 121 FEIRTTDDLTEAWLQEKLSFFR 142

DB 121 FEIRTTDDLTEAWLQEKLSFFR 142

RESULT 7
 AAB58304
 ID AAB58304 standard; Protein: 147 AA.

XX AAB58304;

XX 14-MAR-2001 (first entry)

XX Lung cancer associated polypeptide sequence SEQ ID 642.

XX Human: lung cancer associated protein; neuroprotective; cytostatic;
 KW cardioactive; immunomodulatory; muscular active; vunerary;
 KW gastrointestinal; nephrotoxic; antiinfective; gynecological;
 KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
 KW proliferative disorder; wound healing; infectious disease.

XX Homo sapiens.

XX WO200055180-A2.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US05918.

XX 12-MAR-1999; 99US-0124270.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (ROSE/) ROSEN C A.

XX Ruben SM;

XX WPI; 2000-587514/55.

XX N-PSDB; AAF18180.

XX Lung cancer associated gene sequences, referred to as lung cancer
 PT antigens, useful for treatment, prevention, and diagnosis of disorders
 PT such as lung cancer -
 PS Claim 11; Page 1140-1141; 1425pp; English.

XX polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
 CC associated proteins represented in AAB58106 - AAB58548. Lung cancer
 CC associated proteins and polynucleotide sequences, their agonists, and
 CC antagonists may have neuroprotective; cytostatic; cardioactive;

CC immunomodulatory; muscular active general; vulnereary; gastrointestinal
 CC general; nephrotic; antineoplastic; gynecological; or antibacterial
 CC activity. The invention also includes antibodies specific for the
 CC protein or polynucleotide sequences. The lung cancer associated
 CC polynucleotide sequences may be used for detection of lung cancer,
 CC chromosome identification, as chromosome markers, and for numerous other
 CC diagnostic or research purposes. The proteins may be used to treat
 CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders. The proteins may also be used in the treatment of wounds and
 CC infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and
 CC peptide AAB58549 are used in the course of the invention for the
 CC identification and characterization of the polynucleotide and protein
 CC sequences.

XX Sequence 147 AA;

Query Match 95.1%; Score 699; DB 21; Length 147;

Best Local Similarity 99.3%; Pred. No. 7.3e-70;

Matches 135; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 VCEVDPETLTKRFRKFTDNNALIMKVKDROMVLEEFQNISPEELKMLPEROP 66

Db 12 VCEVDPETLTKRFRKFTDNNALIMKVKDROMVLEEFQNISPEELKMLPEROP 71

Qy 67 RFFVYSKYVHDDGRVSYPLCFIFSSPYGCKPEOQMMYAGSKNRLVQTAELTKVFEIRTT 126

Db 72 RFFVYSKYVHDDGRVSYPLCFIFSSPYGCKPEOQMMYAGSKNRLVQTAELTKVFEIRTT 131

Qy 127 DDLTEAMLQEKLSFFR 142

Db 132 DDLTEAMLQEKLSFFR 147

RESULT 8

ID AAR43941 standard; Protein; 155 AA.

XX AAR43941;

DT 25-MAR-2003 (updated)

DT 10-JUN-1994 (first entry)

DE Human Gli4 Maturation Factor.

XX GMF, neuron; glial cell; nervous system; regeneration; brain tumour;

KM growth factor.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Protein 15..155

FT /label= GMF

FT /note= "Met(14) corresponds to probable

XX US5270452-A.

PD 14-DEC-1993.

XX 31-OCT-1991; 91US-0785185.

XX 28-NOV-1988; 88US-0276847.

PR 26-APR-1991; 91US-0692772.

PR 31-OCT-1991; 91US-0785185.

XX (RHON) RHONE POULENC RORER PHARM INC.

XX (IOWA) UNIV IOWA STATE RES FOUND.

XX Jaye M, Kaplan R, Lim R;

XX WPI; 1993-405019/50.

DR N-PSDB; AA053862.

XX Recombinant glia maturation factor useful for treating abnormal
 PT development of the nervous system - is obtd. by expression of
 PT cDNA obtd. from a human brain stem cDNA library using transformed
 PT host cells

XX Claim 1; Fig 7; 12pp; English.

CC The human GMF sequence was deduced from a cDNA sequence obtained
 CC by screening a human brain stem library with a probe based on a
 CC bovine GMF tryptic fragment. Assuming that translation of GMF mRNA
 CC is initiated at the first ATG codon (see Features Table), the deduced
 CC protein is calculated to have a mol. wt. of 16716. GMF may be useful
 CC to treat injuries to the brain, spinal cord and nerves, to treat
 CC abnormal development of the nervous system and to arrest or reverse
 CC nervous system degeneration and the progress of tumours.
 CC (Updated on 25-MAR-2003 to correct PF field.)

CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 155 AA;

Query Match 83.8%; Score 616; DB 14; Length 155;

Best Local Similarity 81.6%; Pred. No. 1.4e-60;

Matches 115; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MSDSLVCEVDPETLTKRFRKFTDNNALIMKVKDROMVLEEFQNISPEELKME 60

Db 14 MSELIVCDVADVEDLVEKIRKFRFAKETNNALIMKIDKRLVLDLELSISDELKDE 73

Qy 61 LPERQPRFVYSKYVHDDGRVSYPLCFIFSSPYGCKPEOQMMYAGSKNRLVQTAELTKV 120

Db 74 LPERQPRFVYSKYVHDDGRVSYPLCFIFSSPYGCKPEOQMMYAGSKNRLVQTAELTKV 133

Qy 121 FEIRTTDDLTEAMLQEKLSFF 141

Db 134 FEIRTTDDLTEAMLQEKLSFF 154

RESULT 9

ID ABG19927 standard; Protein; 178 AA.

XX ABG19927;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #19918.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

PD 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS84114.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

PS	Claim 20; SEQ ID NO 50286; 103pp; English.
XX	
CC	The invention relates to isolated polynucleotide (I) and
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC	and gene mapping, and in recombinant production of (II). The
CC	polynucleotides are also used in diagnostics as expressed sequence tags
CC	for identifying expressed genes. (I) is useful in gene therapy techniques
CC	to restore normal activity of (II) or to treat disease states involving
CC	(II). (II) is useful for generating antibodies against it, detecting or
CC	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	a food supplement. (II) and its binding partners are useful in medical
CC	imaging of sites expressing (II). (I) and (II) are useful for treating
CC	disorders involving aberrant protein expression or biological activity.
CC	The polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. ABG00010-ABG30377 represent novel human
CC	diagnostic amino acid sequences of the invention.
CC	Note: The sequence data for this patent did not appear in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences .
SO	
XX	Sequence 178 AA:
XX	
XX	Query Match 77.6%; Score 570; DB 22; Length 178;
XX	Best Local Similarity 84.1%; Pred. No.2.3e-55;
XX	Matches 122; Conservative 2; Mismatches 15; Indels 6; Gaps 5
OY	2 SDSLVCVDEDELTEKLRFRFRKRTDAAIIMKYDKDR-QMNVLEEFQNISPE-ELKM 59
Db	 25 SDSLVCVDEDELTEKLRFRFRKRTDAAIIMKYDKDRGMNVLEEFQNISPEORELKM 84
OY	60 ELPER-ORPFWYSKKYVHDDGRVSRPLCTIF-SSPVGCKRPQOMMYAGSKRNLVOTAEI 117
Db	 85 GPRRDKRFYVYSKIVYHDDGRVSRPLCTIFPRPVGCKRPQOMMYAGSKRNLVOTAEI 144
OY	118 TKVEFIRTTDIT--EAMVLOEKLP 140
Db	 145 TKGVPRKSRITYLTLRPLWLOEKLP 169
XX	
XX	RESULT 10
XX	AAV36208
XX	AAV36208 standard: protein; 109 AA.
XX	AAV36208;
XX	
DT	23-SEP-1999 (first entry)
XX	
DE	Human secreted protein #80.
XX	
KW	Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic;
XX	diagnostic; gene therapy; chromosome mapping; secretion vector.
OS	
XX	Homo sapiens.
XX	
PN	WO9925825-A2.
XX	
PD	27-MAY-1999.
XX	
PE	13-NOV-1998; 98WO-IB01862.
XX	
PR	04-SEP-1998; 98US-0099273.
PR	13-NOV-1997; 97US-006677.
PR	17-DEC-1997; 97US-0069957.
PR	09-FEB-1998; 98US-0074121.
PR	13-APR-1998; 98US-0081563.
PR	10-AUG-1998; 98US-0096116.
XX	
PA	(GEST) GENSET.

XX	Bougueleret L, Duclert A, Dumas Milne Edwards J;
PI	WP1: 1999-347472/29.
DR	N-PSDB: AAX97892.
XX	
XX	Extended cDNAs encoding secreted proteins
PS	Claim 7; Page 302; 307pp; English.
XX	
CC	AA36129-Y36222 represent novel human secreted proteins encoded by the
CC	extended cDNA sequences represented in AAX97813-X97906. The proteins
CC	of the invention have cytosolic, thrombotic and osteopathic activity.
CC	The extended cDNAs can be used to express secreted proteins or parts of
CC	them or to obtain antibodies capable of binding to the secreted
CC	proteins. They may also be used in diagnostic, forensic, gene therapy
CC	and chromosome mapping procedures. Uses also include design of
CC	expression vectors and secretion vectors.
SQ	Sequence 109 AA;
Query Match	75.9%; Score 558; DB 20; Length 109;
Best Local Similarity	98.2%; Pred. No. 2,6e-54;
Matches 107; Conservative	1; Mismatches 1; Indels 0; Gaps 0;
QY	34 MKVDKDRQMVYLEEFONISPEELKMELEPEROPFVYVYKYVDDGRVSYPLCFIRSSP 93
Db	1 MKVDKDRQMVYLEEFNRIISPEELKMELEPERQPFVYVYKYVDDGRVSYPLCFIRSSP 60
QY	94 VGCPREQOMYAGSKNRLVQTAELTKYFEIRTTDDLTLEAMLOEKLSPFR 142
Db	61 VGCPREQOMMYAGSKNRLVQTAELTKYFEIRTTDDLTLEAMLOEKLSPFR 109
RESULT 11	
ABG19926	
ID	ABG19926 standard; Protein: 126 AA.
XX	
AC	ABG19926;
XX	
DT	18-FEB-2002 (first entry)
XX	
DE	Novel human diagnostic protein #1917.
XX	
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW	Food supplement; medical imaging; diagnostic; genetic disorder.
XX	
OS	Homo sapiens.
XX	
PN	WO200175067-A2.
XX	
PD	11-OCT-2001.
XX	
PF	30-MAR-2001; 2001WO-US08631.
XX	
PR	31-MAR-2000; 2000US-0540217.
PR	23-AUG-2000; 2000US-0649167.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Drimnac RT, Liu C, Tang YT;
XX	
DR	WP1: 2001-639362/73.
DR	N-PSDB: AAS84113.
XX	
XX	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity -
PS	Claim 20; SEQ ID No 50285; 103pp; English.
XX	
CC	The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (I) is useful for generating antibodies against it, detecting or
CC quantifying a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAG00010-ABG3037 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
CC
CC

Sequence 126 AA:
Query Match 69.9%; Score 513.5; DB 22; Length 126;
Best Local Similarity 78.5%; Pred. No. 2.9e-49;
Matches 106; Conservative 0; Mismatches 4; Indels 25; Gaps 2;

QY 1 MSDSLVCEVDELTETKLRFRFRKRTNNAATIMVKDRQMVLEEFQNSPELKE 60
DB 6 MSDSLVCEVDELTETKLRFRFRKRTNNAATIMVKDRQMVLEEFQ----- 55
QY 61 LPEROPRFVYVSYKYVHDDGRVSYPLCFIFSSPGCKPEQOMYAGSKNRLVQTALTRY 120
DB 56 -----FVYVSYKYVHDDGRVSYPLCFIFSSPGCKPEQOMYAGSKNRLVQTALTRY 108
QY 121 FEIRTTDTLTEAMLQ 135
DB 109 -----QTGMMLQ 115

RESULT 12
AAG03953
ID AAG03953 standard; Protein; 116 AA.
XX
AC AAG03953;
DT 06-OCT-2000 (first entry)
DE Human secreted protein, SEQ ID NO: 8034.
XX
KW Human: 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KM gene therapy; chromosome mapping.
XX
OS Homo sapiens.
XX PN EP1033401-A2.
XX PD 06-SEP-2000.
XX PF 21-FEB-2000; 2000EP-0200610.
XX PR 26-FEB-1999; 99US-0122487.
XX PA (GEST) GENSET.
PI Dumas Milne Edwards J, Duclert A, Giordano J;
DR N-PSDB; AAG03959.
XX
XX WPI; 2000-500381/45.
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -

XX
PS Claim 13; SEQ ID 8034; 71pp + CD-ROM; English.

XX The present sequence is a polypeptide encoded by one of a large number
CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
CC were prepared from total human RNAs or polyA+ RNAs derived from 30
CC different tissues. EST sequences usually correspond mainly to the 3'
CC untranslated region (UTR) of the mRNA because they are often obtained
CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
CC those cases where longer cDNA sequences have been obtained, the full 5'
CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
CC ends and can therefore be used to obtain full length cDNAs and genomic
CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
CC chromosome mapping procedures. They are used to obtain upstream
CC regulatory sequences and to design expression and secretion vectors.
CC
CC

Sequence 116 AA:
Query Match 63.2%; Score 464.5; DB 21; Length 116;
Best Local Similarity 79.3%; Pred. No. 7.6e-44;
Matches 88; Conservative 13; Mismatches 9; Indels 1; Gaps 1;

QY 1 MSDSLVCEVDELTETKLRFRFRKRTNNAATIMVKDRQMVLEEFQNSPELKE 60
DB 1 MSELXVCDVADLVEKLRFRFRKRTNNAATIMKIDKORLVLDDELEGISPELKE 60
QY 61 LPEROPRFVYVSYKYVHDDGRVSYPLCFIFSSPGCKPEQOMYAGSKNR 110
DB 61 LPEROPRFVYVSYKYVHDDGRVSYPLCFIFSSPGCKPEQOMYAGSKNR 111

RESULT 13
ABB61879
ID ABB61879 standard; Protein; 141 AA.
XX
AC ABB61879;
DT 26-MAR-2002 (first entry)
DE Drosophila melanogaster polypeptide SEQ ID NO 12429.
XX
KW Drosophila: developmental biology; cell signalling; insecticide;
KM pharmaceutical.
XX
OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US09231.
XX PR 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.
XX PA (PEKE) PE CORP NY.
PI Venter JC, Adams M, Li PWD, Myers EW;
DR N-PSDB; ABL05982.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Disclosure: SEQ ID NO 12429; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of

CC	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	a food supplement. (II) and its binding partners are useful in medical
CC	imaging of sites expressing (II). (I) and (II) are useful for treating
CC	disorders involving aberrant protein expression or biological activity.
CC	The polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. ABG00010-ABG30377 represent novel human
CC	diagnostic amino acid sequences of the invention.
CC	Note: The sequence data for this patent did not appear in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 58 AA:
Query Match	33.7%; Score 247.5; DB 22; Length 58;
Best Local Similarity	45.7%; Pred. No. 4.8e-20;
Matches 58; Conservative 0; Mismatches 0; Indels 69; Gaps 1	
OY	16 EKLKRFRRKETDNNAIIMKYDKDRQVYLEEFPONISPEELKMELPEROPRPVYSXY 75 1 EKLKRFRRKETDNNAIIMKYDKDRQVYLEEFPQ----- 35
Dd	76 VHDGRVSYPLCFITSSPYGGCKPEQQMAYAGSKNRLVQTAEILKVFETRTDDLTPEAWIQ 135 36 -----VFETRTDDLTPEAWIQ 51
Oy	136 EKLSFPR 142
Dd	52 EKLSFPR 58
RESULT 15	
ABG19925	
ID	ABG19925 standard; Protein; 46 AA.
XX	
AC	ABG19925;
XX	
DT	18-FEB-2002 (first entry)
XX	
DE	Novel human diagnostic protein #19916.
XX	
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX	food supplement; medical imaging; diagnostic; genetic disorder.
OS	Homo sapiens.
XX	
PN	WO200175067-A2.
PD	
PD	11-OCT-2001.
PF	
PF	30-MAR-2001; 2001MO-US08631.
FR	
FR	31-MAR-2000; 2000US-0540217.
FR	23-AUG-2000; 2000US-0649167.
PA	(HYSE-) HYSEQ INC.
XX	
PI	Dmanac RT, Liu C, Tang YT;
XX	
DR	WPI; 2001-639362/73.
DR	N-PSDB; AAS84112.
XX	
PT	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity -
PS	Claim 20; SEQ ID NO 50284; 103pp; English.
XX	
CC	The invention relates to isolated polynucleotide (I) and
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG03377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.

XX
 SQ Sequence 46 AA;

Query Match 22.7%; Score 167; DB 22; Length 46;
 Best Local Similarity 97.1%; Pred. No. 3.3e-11;
 Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 MKVDRQMYVLEEFQNIISPBLKMLPERQPR 67
 ||||||| ||||||| ||||||| ||||||| |||||||
 Db 1 MKVDRQMYVLEEFQNIISPBLKMLPERQPR 34

Search completed: September 23, 2003, 15:08:48
 Job time : 89 secs

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OM protein - protein search, using sw model

Run on: September 23, 2003, 15:06:08 ; Search time 41 Seconds
(without alignments)
333.072 Million cell updates/sec

Title: US-10-004-832-2

Perfect score: 735

Sequence: 1 MSDSLVCEVPELLEKLRK.....IRTTDDLTEAMLQEKLSFPR 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	686	93.3	142	2 JC7218	glia maturation fa
2	622	84.6	142	1 PT0410	glia maturation fa
3	617	83.9	141	1 JDBOB	glia maturation fa
4	611	83.1	141	1 S22149	glia maturation fa
5	349	47.5	138	2 JC6308	glia maturation fa
6	175	23.8	141	2 T37877	cofilin/tropomyosi
7	123.5	16.8	328	2 T40910	probable tyrosine
8	116.5	15.9	149	2 S54047	hypothetical prote
9	113	15.4	350	2 A55922	tyrosine kinase A6
10	111.5	15.2	133	2 T01232	actin-depolymerizi
11	111.5	15.2	140	2 A86149	actin-depolymerizi
12	109	14.8	139	2 S30935	actin-depolymerizi
13	109	14.8	139	2 T46362	actin-depolymerizi
14	106.5	14.5	357	2 T30015	probable tyrosine
15	103.5	14.1	133	2 T47539	actin depolymerizi
16	100.5	13.7	130	2 T05788	actin-depolymerizi
17	97.5	13.3	142	2 S71361	actin-binding prot
18	95.5	13.0	130	2 T05767	actin-depolymerizi
19	95	12.9	130	2 T47540	actin-depolymerizi
20	93	12.7	132	2 G64717	actin depolymerizi
21	92.5	12.6	137	2 T43245	probable actin-dep
22	91	12.4	126	2 S30934	actin-depolymerizi
23	91	12.4	1289	2 F72308	hypothetical prote
24	90.5	12.3	332	2 S64375	probable tyrosine
25	85.5	11.6	139	2 T02914	actin-depolymerizi
26	84	11.4	132	2 B84543	actin depolymerizi
27	82.5	11.2	166	1 S12632	cofilin - human
28	82.5	11.2	166	1 S12584	cofilin - mouse
29	82.5	11.2	166	2 S49101	cofilin - rat

30	80.5	11.0	166	1 A29240	cofilin - pig
31	80.5	11.0	427	2 B71466	hypothetical prote
32	80.5	11.0	520	2 F70350	recombination prot
33	79	10.7	165	1 A35702	desitin - chicken
34	78.5	10.7	166	1 A35812	cofilin, muscle -
35	77.5	10.5	139	2 T02883	actin-depolymerizi
36	77.5	10.5	379	2 T34100	hypothetical prote
37	77	10.5	771	2 H69305	signal-transducing
38	76.5	10.4	609	2 S57378	hypothetical prote
39	76	10.3	139	2 T02882	actin-depolymerizi
40	76	10.3	875	2 JC5186	DNA-directed DNA p
41	75.5	10.3	165	1 A54184	desitin [validated
42	75.5	10.3	165	1 A35179	desitin - pig
43	75.5	10.3	166	1 B35703	cofilin - chicken
44	75.5	10.3	349	2 B83973	hypothetical prote
45	75.5	10.3	510	2 T20276	hypothetical prote

ALIGNMENTS

RESULT 1

JC7218 glia maturation factor-gamma - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 02-Nov-2001

C:Accession: JC7218

R:Tsukikl, H.; Asai, K.; Yamamoto, M.; Fujita, K.; Inoue, Y.; Kawai, Y.; Tada, T.; Mor

J. Biochem. 127, 517-523, 2000

A:Title: Cloning of a rat glia maturation factor-gamma(RGMEG) cDNA and expression of

A:Reference number: JC7218; MUID:20198266; PMID:10731725

A:Accession: JC7218

A:Molecule type: mRNA

A:Residues: 1-142 <TSU>

C:Comment: This factor is a regulator of signal transduction with many phosphorylatio

C:Superfamily: glia maturation factor beta

C:Keywords: differentiation

Query Match

Best Local Similarity 93.3%; Score 686; DB 2; Length 142;

Matches 130; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY	1	MSDSLVCVPELLEKLRKFRFPEDNNAITIKVDRQVYVEEFQNSPELKE	60
DB	1	MSDSLVCVDPPELKEITLKRFRKETNNAAITIKVDRQVYVEEFQNSPELKE	60
QY	61	LPERPFRVVSYSKYVHDGRVSYPLCFIFSSPYGCKPEQOMYAGSKNRLVQTAELTKV	120
DB	61	LPERPFRVVSYSKYVHDGRVSYPLCFIFSSPYGCKPEQOMYAGSKNRLVQIAELTKV	120
QY	121	FEIRTTDDLTEAMLQEKLSFPR	142
DB	121	FEIRTTDDLNETWLEKLAFFR	142

RESULT 2

PT0410 glia maturation factor beta - human

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Sep-1999

C:Accession: PT0410

J:Kaplan, R.; Zaher, A.; Jave, M.; Lim, R.

J. Neurochem. 57, 483-490, 1991

A:Title: Molecular cloning and expression of biologically active human glia maturation

A:Reference number: PT0410; MUID:91303115; PMID:1712830

A:Accession: PT0410

A:Molecule type: mRNA

A:Residues: 1-142 <KAP>

A:Cross-references: GB:M66492; GB:M31742; NID:q183369; PIDN:AAA5614.1; PID:q183370

C:Comment: This protein promotes the differentiation of normal neurons and glial cell

C:Genetics:

A:Gene: GDB:GMFB

A:Cross-references: GDB:134671

C:Superfamily: glia maturation factor beta

Query Match 84.6%; Score 622; DB 1; Length 142;
Best Local Similarity 82.3%; Pred. No. 1.4e-50;
Matches 116; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

QY 1 MSDSLVCEVDEPDELTEKLRFRFRKRTDAAIIMKVDKRDQNVLEEFQNIISPEELKME 60
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 1 MSESIVCDVADLVLEKLRFRFRKRTNNAIIMKIDKRLVLDLEEGISPELKDDE 60
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|

QY 61 LPEROPRFVYVSYKVVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAEITKV 120
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 61 LPEROPRFVYVSYKVVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAEITKV 120
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|

QY 121 FEIRTTDDLTEAMLQELKLSFF 141
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 121 FEIRTTDDLTEAMLREKLGFF 141
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|

RESULT 3

JDBoB glia maturation factor beta - bovine

C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 05-Aug-1994
C:Accession: A33102; A33066; A60210

R:Lim, R.; Zaher, A.; Lane, W.S.

Proc. Natl. Acad. Sci. U.S.A. 87, 5233-5237, 1990

A:Title: Complete amino acid sequence of bovine glia maturation factor beta.

A:Reference number: A33102; MUID:90319086; PMID:2196564

A:Accession: A33102

A:Molecule type: protein

A:Residues: 1-141 <LIM>

C:Comment: This protein causes differentiation of brain cells, stimulation of neural reg

C:Superfamily: glia maturation factor beta

C:Keywords: acetylated amino end; growth factor

F:1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 83.9%; Score 617; DB 1; Length 141;
Best Local Similarity 82.1%; Pred. No. 4e-50;
Matches 115; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

QY 2 SDSLVCEVDEPDELTEKLRFRFRKRTDAAIIMKVDKRDQNVLEEFQNIISPEELKME 61
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 1 SESLVCDVADLVLEKLRFRFRKRTNNAIIMKIDKRLVLDLEEGISPELKDDE 60
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|

QY 62 PEROPRFVYVSYKVVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAEITKV 121
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 61 PEROPRFVYVSYKVVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAEITKV 120
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|

QY 122 EIRTTDDLTEAMLQELKLSFF 141
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 121 EIRTTDDLTEAMLREKLGFF 140
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|

RESULT 4

S22149 glia maturation factor beta - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

C:Accession: S22149

R:Zaher, A.

submitted to the EMBL Data Library, December 1991

A:Reference number: S22149

A:Accession: S22149

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-141 <ZAH>

A:Cross-references: EMBL:Z11558; NID:956294; PID:g1334282

C:Superfamily: glia maturation factor beta

Query Match 83.1%; Score 611; DB 1; Length 141;
Best Local Similarity 80.7%; Pred. No. 1.5e-49;
Matches 113; Conservative 16; Mismatches 11; Indels 0; Gaps 0;

QY 2 SDSLVCEVDEPDELTEKLRFRFRKRTDAAIIMKVDKRDQNVLEEFQNIISPEELKME 61
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 1 SESLVCDVADLVLEKLRFRFRKRTNNAIIMKIDKRLVLDLEEGISPELKDDE 60
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|

QY 62 PEROPRFVYVSYKVVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAEITKV 121
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 61 PEROPRFVYVSYKVVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAEITKV 120
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|

QY 122 EIRTTDDLTEAMLQELKLSFF 141
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 121 EIRTTDDLTEAMLREKLGFF 140
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|

RESULT 5

JC6308 glia maturation factor - nematode (Brugia malayi)

C:Species: Brugia malayi

C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 17-Mar-1999

C:Accession: JC6308

R:Lim, L.X.; Xu, H.; Weller, P.F.; Shi, A.; Debnath, I.

Gene 186, 1-5, 1997

A:Title: Structure and expression of a novel filarial gene for glia maturation factor

A:Reference number: JC6308; MUID:97199361; PMID:9047337

A:Accession: JC6308

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-138 <LIU>

A:Cross-references: GB:062806

C:Superfamily: glia maturation factor beta

Query Match 47.5%; Score 349; DB 2; Length 138;
Best Local Similarity 44.9%; Pred. No. 2.7e-25;
Matches 62; Conservative 35; Mismatches 41; Indels 0; Gaps 0;

QY 1 MSDSLVCEVDEPDELTEKLRFRFRKRTDAAIIMKVDKRDQNVLEEFQNIISPEELKME 60
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 1 MTDALKEICELVADLVLEKLRFRFRKRTNNAIIMKIDKRLVLDLEEGISPELKDDE 60
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|

QY 61 LPEROPRFVYVSYKVVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAEITKV 120
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 61 LPVDDPRIVISTYERVHDDGRVSYPLSLVIFSPGCKPQLMMYAGSKNRLVQTAEITKV 120
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|

QY 121 FEIRTTDDLTEAMLQELK 138
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 121 FEIRTTDDLTEAMLREK 138
||:||||:| :| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|

RESULT 6

T37877 cofilin/tropomyosin-type actin binding protein - fission yeast (Schizosaccharomyces p

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000

C:Accession: T37877

R:Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, August 1997

A:Reference number: Z21751

A:Accession: T37877

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-141 <SKR>

A:Cross-references: EMBL:Z98597; PIDN:CAB11220.1; GSPDB:GN00066; SPDB:SPAC17H9.11

A:Experimental source: strain 972h-; cosmid c17H9

C:Genetics:

A:Gene: SPAC17H9.11

A:Map position: 1

C:Superfamily: glia maturation factor beta

Query Match 23.8%; Score 175; DB 2; Length 141;
Best Local Similarity 32.9%; Pred. No. 3.7e-09;
Matches 46; Conservative 29; Mismatches 63; Indels 2; Gaps 2;

QY 1 MSDSLVCEVDEPDELTEKLRFRFRKRTDAAIIMKVDKRDQNVLEEFQNIISPEELK 58

Db 1 MSESEAMFTISDPTMKMEIDRFRLRLKKSVMYAFILKVDKATKTEIYVDGIMDLQSTEEVA 60
 QY 59 MELPEROPRVVYKYKVVHDDGRVSYPLCFIFSSPGCKPEQOMMYAGSKNRLVOTAEILT 118
 61 DELSEINPRFLIVSYPTKTGRLSTPLFMIVWRPSPATPNDLSMTIYASAKVMFQDVSQVH 120
 QY 119 KVFETRTDDLTETAMLOEKL 138
 121 KVFETRTDDLTETAMLOEKL 140

RESULT 7

T40910
 Probable tyrosine kinase - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Dec-2002
 C:Accession: T40910
 R:Murphy, L.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, December 1998
 A:Reference number: Z21956
 A:Accession: T40910
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-328 <MUR>
 A:Cross-references: EMBL:AL034490; PIDN:CAA22475.1; GSPDB:GN00068; SPDB:SPCC126.06
 C:Experimental source: strain 97zh-; cosmid c126
 C:Genetics:
 A:Gene: SPDB:SPCC126.06
 A:Map position: 3
 A:introns: 9/1; 35/1; 157/3; 200/3; 246/1; 285/3
 C:Superfamily: probable tyrosine kinase

Query Match 16.8%; Score 123.5; DB 2; Length 328;
 Best Local Similarity 29.5%; Pred. No. 0.00059;
 Matches 39; Conservative 28; Mismatches 50; Indels 15; Gaps 7;

QY 6 VVCEVDPELTETKLRFRFKETDNNAILMKVNDKQMVLEEFQNPISPEELKMLPERQ 65
 174 VAMSIDDKALKALSD--LKSTENMLVILSIDK--EVLISQEKQNPISPDVKSFFSSTE 229
 QY 66 PRFVVSYSKYVVDGRVSYPLCFIFSSPGCKPEQOMMYAGSKNRLVOT--AELTKVEE- 122
 230 PWFARVYS--LPKDG--SSKILFIYICPMQATVKRMVYSSSKLGLDSIKRELGLVIDG 284
 QY 123 -IRITD--DLTE 131
 285 KIESNDADITE 296

RESULT 8

S54047
 hypothetical protein YDR063w - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein D4245; hypothetical protein D4249; hypothetical
 C:Species: Saccharomyces cerevisiae
 C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
 C:Accession: S54047; S58843; S61752; S67879
 R:Hunt, S.; Bowman, S.; Harris, D.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: S54031
 A:Accession: S54047
 A:Molecule type: DNA
 A:Residues: 1-149 <HUN>
 A:Cross-references: EMBL:Z49209; NID:g798897; PIDN:CAA89092.1; PID:g798914
 R:Brandt, P.; Otto, B.; Ramlow, S.; Blocker, H.
 submitted to the EMBL Data Library, January 1995
 A:Reference number: S58832
 A:Accession: S58843
 A:Molecule type: DNA
 A:Residues: 1-149 <BRA>
 A:Cross-references: EMBL:X84162; NID:g706817; PIDN:CAA58979.1; PID:g706829
 R:Brandt, P.; Ramlow, S.; Otto, B.; Blocker, H.
 yeast 12, 85-90, 1996

A:Title: Nucleotide sequence analysis of a 32,500 bp region of the right arm of Sacch
 A:Reference number: S61741; MUID:96381250; PMID:8789263
 A:Accession: S61752
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-149 <BRW>
 A:Cross-references: EMBL:X84162; NID:g706817; PIDN:CAA58979.1; PID:g706829
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
 R:Blocker, H.; Brandt, P.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S67587
 A:Accession: S67879
 A:Molecule type: DNA
 A:Residues: 1-149 <BLW>
 A:Cross-references: EMBL:Z74359; NID:g1431514; PIDN:CAA98881.1; PID:g1431515; MIPS:YD
 A:Experimental source: strain S288C
 C:Genetics:
 A:Cross-references: SGD:S0002470
 A:Map position: 4R
 C:Superfamily: g1a maturation factor beta

Query Match 15.9%; Score 116.5; DB 2; Length 149;
 Best Local Similarity 27.7%; Pred. No. 0.001;
 Matches 39; Conservative 30; Mismatches 61; Indels 11; Gaps 6;

QY 9 EVDPELTETKLRFR-FKRETDN-AALIMKVD-KDQMVLEEFQNPISPE-----ELKME 60
 6 KIGTETRNKIKKFKETSTARTSIDKLSIKIEKPSYEIVDEDEQEEDEIDELSELAEI 65
 QY 61 IPEROPRVVYKYKVVHDDGRVSYPLCFIFSSPGV-CKPEQOMMYAGSKNRLVOTAEILT 119
 66 LPDNPFRVLRVLRPTTADGFRKQTPVLVYKPMIVSQEKMLYAGALEMIRECGTFK 125
 Db 120 VFEIRT--TDLTETAMLOEKL 138
 126 LIEVSSGLEDDSDVEELREQL 146

RESULT 9

A55922
 tyrosine kinase A6 - human
 C:Species: Homo sapiens (man)
 C:Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 09-Dec-2002
 C:Accession: A55922
 R:Beeler, J.F.; Laroche, W.J.; Chedid, M.; Tronick, S.R.; Aaronson, S.A.
 Mol. Cell. Biol. 14, 982-988, 1994
 A:Title: Prokaryotic expression cloning of a novel human tyrosine kinase.
 A:Reference number: A55922; MUID:94119116; PMID:7507208
 A:Accession: A55922
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-350 <BEB>
 A:Cross-references: GB:U02680; NID:g451481; PIDN:MAC50062.1; PID:g451482
 C:Superfamily: probable tyrosine kinase

Query Match 15.4%; Score 113; DB 2; Length 350;
 Best Local Similarity 26.4%; Pred. No. 0.006;
 Matches 38; Conservative 33; Mismatches 53; Indels 20; Gaps 7;

QY 6 VVCEVDPELTETKLRFRFKETDNNAILMKVNDKQMVLEEFQNPISPEELKMLPERQ 65
 178 VAFPSRAFOALELNNRQLN--YVLEIDIKNEIIL-----ANTNTELK-DLPKRI 229
 QY 66 P---RFVVSYSKYVVDGRVSYPLCFIFSSP-VGCKPEQOMMYAGSKNRLVOTAE--- 116
 230 PKDSARYHEFLYKSH-EGDYLESIVFISMPGYCISIREMLVSSCKSLLEIVERQLQ 288
 QY 117 --LTKVEFIRTTDDLTETAMLOEKL 138
 289 MDVIRKIKIENDGDELTADELVEEV 312

RESULT 10

Db 293 KKEIGDGAELTAFLYDEV 312

RESULT 14

T30015

probable tyrosine kinase F38E9.5 [similarity] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Dec-2002

C:Accession: T30015

R:Wu, X.; Gattung, S.

submitted to the EMBL Data Library, January 1996

A:Description: The sequence of C. elegans cosmid F38E9.

A:Reference number: 220722

A:Accession: T30015

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-357 <WUX>

A:Cross-references: EMBL:U46668; PIDN:AAA93345.1; CESP:F38E9.5

C:Genetics:

A:Gene: CESP:F38E9.5

A:Introns: 9/1; 83/2; 123/3; 169/3; 197/3; 248/1; 288/3; 312/3

C:Superfamily: probable tyrosine kinase

Query Match

Best Local Similarity 14.5%; Score 106.5; DB 2; Length 357;

Matches 37; Conservative 30; Mismatches 60; Indels 35; Gaps 5;

QY 6

171 VAFVDPVRLTEKRFRRKFTDNNALIMKVDKROMVYLEEFQNI-----SPEELKMELEPERQ 65

171 VAFVDPVRLTEKRFRRKFTDNNALIMKVDKROMVYLEEFQNI-----SPEELKMELEPERQ 65

QY 66

228 PRITFYNDHW-EGVPOQCTLFYSLPSSGSSIKERMYSCKGPFLSAAGNOXGVVIT 286

QY 117

287 NKFLQKRSNMKFKIREKIFLRLKNDMEVDARDLSEKALLE 328

RESULT 15

T47539

actin depolymerizing like protein - Arabidopsis thaliana

N:Alternate names: protein F16L2.200

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000

C:Accession: T47539

R:Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, S.;

submitted to the Protein Sequence Database, March 2000

A:Reference number: 224468

A:Accession: T47539

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-133 <JOR>

A:Cross-references: EMBL:AL162459

A:Experimental source: cultivar Columbia; BAC clone F16L2

C:Genetics:

A:Map position: 3

A:Introns: 43/1; 84/2

A:Note: F16L2.200

C:Superfamily: cofillin

Query Match

Best Local Similarity 14.1%; Score 103.5; DB 2; Length 133;

Matches 33; Conservative 30; Mismatches 41; Indels 21; Gaps 6;

QY 13

13 ELTEKLRKFRKFTDNNALIMKVDKROMVYLEEFQNI-----SPEELKMELEPERQ 66

13 ELTEKLRKFRKFTDNNALIMKVDKROMVYLEEFQNI-----SPEELKMELEPERQ 66

QY 67

64 RYALIDIEFVPERKI-----CFIAMSPTAKMKRMKMIYSTIKDRFKRELDGIQV-EFHAT 118

QY 127 DDLTE 131

Db 119 -DLTD 122

Search completed: September 23, 2003, 15:11:51
Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 23, 2003, 14:58:43 : Search time 24 Seconds

(without alignments)
278.241 Million cell updates/sec

Title: US-10-004-832-2

Sequence: 1 MSDSLVCEVCEPELLEKLRK.....IRTTDDLTEAMLOEKLSFR 142

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	735	100.0	142	1	GLMG_HUMAN
2	617	83.9	141	1	GLMB_HUMAN
3	611	83.1	141	1	GLMB_RAT
4	111.5	15.2	140	1	ADPF_ARATH
5	109	14.8	139	1	ADPF_LILLO
6	108	14.7	139	1	ADPF_ARATH
7	105	14.3	139	1	ADPF_ARATH
8	104	14.1	139	1	ADPF_ARATH
9	103	14.0	139	1	ADPF_PETRY
10	100.5	13.7	143	1	ADPF_PETRY
11	97.5	13.3	137	1	ACTP_ACACA
12	95	12.9	137	1	ADPF_ARATH
13	93	12.7	146	1	ADPF_ARATH
14	92.5	12.6	137	1	CORF_SCHPO
15	91.5	12.4	137	1	CORF_DICDI
16	91	12.4	126	1	ADPF_BRANA
17	90.5	12.3	332	1	TWFL_YEAST
18	85.5	11.6	139	1	ADPF_MAIZE
19	84	11.4	143	1	ADPF_ARATH
20	82.5	11.2	166	1	CORF_HUMAN
21	82.5	11.2	166	1	CORF_MOUSE
22	82.5	11.2	166	1	CORF_RAT
23	80.5	11.0	166	1	CORF_PIG
24	80.5	11.0	427	1	RMOC_CHLIR
25	80.5	11.0	520	1	RECNA_AOUAE
26	79.5	10.8	168	1	CORF_XENLA
27	79	10.7	165	1	DEST_CHICK
28	78.5	10.7	166	1	CORF_HUMAN
29	78.5	10.7	166	1	CORF_MOUSE
30	78.5	10.7	166	1	CORF_CHICK
31	77.5	10.5	139	1	ADPF_MAIZE
32	77	10.5	161	1	MPH6_MOUSE
33	76	10.3	139	1	ADPF_MAIZE

34	76	10.3	165	1	DEST_MOUSE
35	76	10.3	875	1	DPOL_SULAC
36	75.5	10.3	165	1	DEST_HUMAN
37	75.5	10.3	168	1	CORF_XENLA
38	73.5	10.0	425	1	RMOC_CHLIR
39	73	9.9	559	1	INXA_CAEEL
40	73	9.9	624	1	HTPG_CLOAB
41	72	9.8	363	1	YGDE_HAEIN
42	71.5	9.7	366	1	ARCD_PYPERU
43	71	9.7	143	1	CORF_YEAST
44	71	9.7	345	1	HRCA_LISIN
45	71	9.7	345	1	HRCA_LISMO

ALIGNMENTS

RESULT 1
ID GLMG_HUMAN STANDARD; PRT; 142 AA.
AC 060234;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Glia maturation factor gamma (GMF-gamma).
GN GMF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98207113; PubMed=9545571;
RA Asai K., Fujita K., Yamamoto M., Hotta T., Morikawa M., Kokubo M.,
RA Moriyama A., Kato T.;
RT "Isolation of novel human CDNA (hGMF-gamma) homologous to Glia
RT Maturation Factor-beta gene";
RL Biochim. Biophys. Acta 1396:242-244(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=98318631; PubMed=9653160;
RA Mao M., Fu G., Wu J.-S., Zhang Q.-H., Zhou J., Kan L.-X., Huang Q.-H.,
RA He K.-L., Gu B.-W., Han Z.-G., Shen Y., Gu J., Yu Y.-P., Xu S.-H.,
RA Wang Y.-X., Chen S.-J., Chen Z.;
RT "Identification of genes expressed in human CD34(+) hematopoietic
RT stem/progenitor cells by expressed sequence tags and efficient full-
RT length cDNA cloning";
RL Proc. Natl. Acad. Sci. U.S.A. 95:8175-8180(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20009844; PubMed=10541589;
RA Peters N., Smith J.S., Tachibana I., Lee H.K., Pohl U., Porter B.P.,
RA Louis D.N., Jenkins R.B.;
RT "The human glia maturation factor-gamma gene: genomic structure and
RT mutation analysis in gliomas with chromosome 19q loss";
RL Neurogenetics 2:163-166(1999).
-!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LUNG, HEART, AND
PLACENTA.
-!- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY. GMF
SUBFAMILY.
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-!- EMBL: AB001993; BAA25572.1; -
DR EMBL; AF038956; AAC39870.1; -

DR EMBL: AF108027; AAD27807.1; -.
 DR EMBL: AF108022; AAD27807.1; JOINED.
 DR EMBL: AF108023; AAD27807.1; JOINED.
 DR EMBL: AF108024; AAD27807.1; JOINED.
 DR EMBL: AF108025; AAD27807.1; JOINED.
 DR EMBL: AF108026; AAD27807.1; JOINED.
 DR Genew: HGNC:4374; GMFB.
 DR MIM: 604104; -.
 DR GO: GO:0008047; F:enzyme activator activity; TAS.
 DR GO: GO:0004860; F:protein kinase inhibitor activity; TAS.
 DR GO: GO:0006468; P:protein kinase inhibitor activity; TAS.
 DR InterPro: IPR002108; Actbind_coflin.
 DR Pfam: PF00241; cofilin_Adf_1.
 DR SMART: SM00102; ADF_1.
 DR Growth factor.
 KW SEQUENCE 142 AA; 16801 MW; DB64BD8DE4F88170 CRC64;

Query Match 100.0%; Score 735; DB 1; Length 142;
 Best Local Similarity 100.0%; Pred. No. 3.2e-60;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSDSLVCEVDEPLETEKLRFRFRKRETDNAIIMKVDKRDQNVYLEEFONISPEELKME 60
 DB 1 MSDSLVCEVDEPLETEKLRFRFRKRETDNAIIMKVDKRDQNVYLEEFONISPEELKME 60
 OY 61 LPERQPRFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTALTKV 120
 DB 61 LPERQPRFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTALTKV 120
 OY 121 FEIRTTDTLEAMLOEKISFF 142
 DB 121 FEIRTTDTLEAMLOEKISFF 142

RESULT 2

GLMB_HUMAN STANDARD: PRT: 141 AA.
 AC P17774;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glia maturation factor beta (GMF-beta).
 GN GMFB.
 OS Homo sapiens (Human), and
 OS Bos taurus (Bovine).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606, 9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=91303115; PubMed=1712830;
 RA Kaplan R., Zahner A., Jaye M., Lim R.;
 RT "Molecular cloning and expression of biologically active human glia
 maturation factor-beta.";
 RL J. Neurochem. 57:483-490(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Brain;
 RA Saito T., Tanaka N., Toyomasu T.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE.
 RC SPECIES=Bovine;
 RX MEDLINE=90319086; PubMed=2196564;
 RA Lim R., Zahner A., Lane W.S.;
 RT "Complete amino acid sequence of bovine glia maturation factor beta.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5233-5237(1990).
 RN [4]
 RP PHOSPHORYLATION.
 RC SPECIES=Human;
 RX MEDLINE=95321959; PubMed=7598724;
 RA Lim R., Zahner A.;

RT "phorbol ester stimulates rapid intracellular phosphorylation of glia
 maturation factor.";
 RL Biochem. Biophys. Res. Commun. 211:928-934(1995).
 CC -I- FUNCTION: THIS PROTEIN CAUSES DIFFERENTIATION OF BRAIN CELLS,
 STIMULATION OF NEURAL REGENERATION, AND INHIBITION OF
 CC PROLIFERATION OF TUMOR CELLS.
 CC -I- PTM: PHOSPHORYLATED; STIMULATED BY PHORBOL ESTER.
 CC -I- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY. GMF
 CC SUBFAMILY.

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 CC or send an email to license@sib-sib.ch).

CC EMBL: M86492; AAS8614.1; -.
 DR EMBL: AB001106; BAA19232.1; -.
 DR PIR: A3102; JDBOB.
 DR PIR: PT0410; PT0410.
 DR Genew: HGNC:4373; GMFB.
 DR MIM: 601713; -.
 DR GO: GO:0008047; F:enzyme activator activity; TAS.
 DR GO: GO:0004860; F:protein kinase inhibitor activity; TAS.
 DR GO: GO:0004871; F:signal transducer activity; TAS.
 DR GO: GO:0007399; P:neurogenesis; TAS.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; TAS.
 DR GO: GO:0007165; P:signal transduction; TAS.
 DR InterPro: IPR002108; Actbind_coflin.
 DR Pfam: PF00241; cofilin_Adf_1.
 DR SMART: SM00102; ADF_1.
 KW Growth factor; Acetylation; Phosphorylation.
 FT INT_MET 0
 FT MOD_RES 1
 FT SEQUENCE 141 AA; 16582 MW; EE1DA4FE200E2F370 CRC64;

Query Match 83.9%; Score 617; DB 1; Length 141;
 Best Local Similarity 82.1%; Pred. No. 1.7e-49;
 Matches 115; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

OY 2 SDSLVCEVDEPLETEKLRFRFRKRETDNAIIMKVDKRDQNVYLEEFONISPEELKME 61
 DB 1 SESLVCDVADVDLEKLRFRFRKRETDNAIIMKVDKRDQNVYLEEFONISPEELKME 60
 OY 62 PERQPRFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTALTKV 121
 DB 61 PERQPRFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTALTKV 120
 OY 122 FEIRTTDTLEAMLOEKISFF 141
 DB 121 FEIRTTDTLEAMLOEKISFF 140

RESULT 3

GLMB_RAT STANDARD: PRT: 141 AA.
 AC O63228;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Glia maturation factor beta (GMF-beta).
 GN GMFB.
 OS Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=93171924; PubMed=8436977;
 RA Zahner A., Fink B.D., Lim R.;
 RT "Expression of glia maturation factor beta mRNA and protein in rat

[illegible]

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RA Sakano H,Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utrackack T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RA "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RA thaliana.";
RA Nature 408:816-820(2000).
RL
CC CC -I- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENTS
CC CC (-ACTIN) AND BINDS TO ACTIN MONOMERS (BY SIMILARITY).
CC CC -I- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
CC CC
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CC CC or send an email to license@isb-sib.ch).
CC CC
CC CC EMBL: AC009273; AAF78408.1;
CC CC PTR: A86149; A86149.
CC CC HSSP: Q39250; I175.
CC CC DR InterPro: IPR002108; Actbind_cofin.
CC CC DR Pfam: PF00241; cofilin_ADF.1.
CC CC DR PRODOM: PD002129; Actbind_cofin.1.
CC CC DR SMART: SM00102; ADF.1.
CC CC DR PROSITE: PS00325; ACTIN_DEPOLYMERIZING.1.
CC CC
CC CC KW Actin-binding; Multigene family
CC CC
CC CC DOMAIN 92 111 ACTIN-BINDING (POTENTIAL).
CC CC SEQUENCE 140 AA; 16341 MW; B9845FF24B657859 CRC64;
CC CC
CC CC
CC CC Query Match 15.2%; Score 111.5; DB 1; Length 140;
CC CC Best Local Similarity 28.1%; Pred. No. 0.0017;
CC CC Matches 34; Conservative 23; Mismatches 43; Indels 21; Gaps 5;
CC CC
CC CC
CC CC QY 13 ELTEKLEKRRPRKRETDNAIIMKYDKRQNVVL-----EEFONISPEELKMELEPRQP 66
CC CC Db 20 ELNAK-RNYRF-----IVPKDEKAQCVIMDKLGNPEYV-----EDFTSIPDEDC 65
CC CC
CC CC QY 67 RFVAVSYKYYVHDGKRVSPICFIFSSVGGCKPEQOMYVASKKNRLVOTAEITVFEIRTT 126
CC CC Db 66 RIVAVYDFTTPENCKQSKFIPLFVMSPDTSRVNSKMLYASSKDRFKRELDGIOY-ELQAT 124
CC CC
CC CC QY 127 D 127
CC CC Db 125 D 125
CC CC
CC CC
CC CC RESULT 5
CC CC ADF_LILLO STANDARD; PRT; 139 AA.
CC CC ID ADF_LILLO
CC CC AC P30175;
CC CC DT 01-APR-1993 (Rel. 25, Created)
CC CC DT 01-APR-1993 (Rel. 25, Last sequence update)
CC CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC CC DE Actin-depolymerizing factor (ADF).
CC CC OS Liliium longiflorum (Trumpet Lily).
CC CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC CC OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;
CC CC OC Liliium.
CC CC OX NCBI_TaxID=4690;
CC CC RN [1]
CC CC RP SEQUENCE FROM N.A.
CC CC RC STRAIN=cv. Nellie white; TISSUE=pollen;
CC CC RX MEDLINE=93144690; PubMed=8425049;
CC CC RA Kim S.-R., Kim Y., An G.;
CC CC RT "Molecular cloning and characterization of another-preferential cDNA
CC CC encoding a putative actin-depolymerizing factor.";
CC CC RL Plant Mol. Biol. 21:39-45(1993).
CC CC
CC CC -I- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENTS
CC CC (-F-ACTIN) AND BINDS TO ACTIN MONOMERS (BY SIMILARITY).
CC CC -I- TISSUE SPECIFICITY: PREFERENTIALLY IN MATURE ANTHR.
CC CC -I- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.

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CC
DR EMBL: Z14110; CAA78483.1; -
DR PIR: S30935; S30935.
DR HSSP: Q39250; 1F7S.
DR InterPro: IPR002108; Actbind_cofln.
DR Pfam: PF00241; cofilin_ADF.1.
DR ProDom: PD002129; Actbind_cofln; 1.
DR SMART: SM00102; ADF.1.
DR PROSITE: PS00325; ACTIN_DEPOLYMERIZING; 1.
KW Actin-binding
FT DOMAIN 92 111 ACTIN-BINDING (POTENTIAL).
FT SEQUENCE 139 AA; 16226 MW; 0B45CC67136F1EA9 CRC64;
SO
Query Match 14.8%; Score 109; DB 1; Length 139;
Best Local Similarity 27.6%; Pred. No. 0.0029;
Matches 37; Conservative 26; Mismatches 53; Indels 16; Gaps 4;
OY 1 MSDSLVCEVDEPLETEK-----RFRFRKETDMAAIIMKVDKROMVYLEEPEQ-NIS 53
DB 1 MANSSGMAVDECKELKFMELKAKRNF-----IVFKIEEVQGVTVERLQGPRES 52
OY 54 PEELKMELEPQRPQVYVSYKYVHDGKVSYPICFTSSPGVCKPEQOMTAGSKNRLVQ 113
DB 53 YDDETECLPNECRVAFDFEDFVENDCQSKSIFIFSWSPITSRVSMTLYASTKDRRK 112
OY 114 TAEITKVEIRPTD 127
DB 113 ELDGIV-ELQATD 125
RESULT 6
ADFL_ARATH STANDARD: PRT; 139 AA.
AC Q39250.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Actin-depolymerizing factor 1 (ADF-1) (AtADF1).
GN ADF1 OR AR3G46010 OR F16L2.220.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC NCB1_taxid=3702;
OX [1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia.
RA Staiger C.J., Ashworth S.L.;
RT "Actin depolymerizing factor from Arabidopsis thaliana severs
RL polymers and binds to monomers in a pH-dependent manner.";
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=cv. Columbia.
RA MEDLINE=21307188; PubMed=11414611;
RA Dong C.-H., Kost B., Xia G., Chua N.-H.;
RT "Molecular identification and characterization of the Arabidopsis
RL AtADF1, AtADF5 and AtADF6 genes.";
RL Plant Mol. Biol. 45:517-527(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia.
RA MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unselid M.,
RA Faltmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,

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RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choisme N., Artiguenave F., Robert C., Brotier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Bernes V.,
RA Wunbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Scharfe M., Schoen O., Barques M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Ducheman D.,
RA Cooke R., Laudie M., Berger-Liauro C., Purnelle B., Masny D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argilou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Radd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts R., Uterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Walts R., Wu D., Peterson J., Van Aken S.,
RA Pal G., Millscher J., Sellers P., Gill J.E., Feldlyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneo T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsunoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shingo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RA "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana.";
RT Nature 408:820-822(2000).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=20481864; PubMed=11025548;
RA Bowman G.D., Nodelman I.M., Hong Y., Chua N.H., Lindberg U.,
RA Schutt C.E.;
RT "A comparative structural analysis of the ADF/cofilin family.";
RT Proteins 41:374-384(2000).
CC -1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERES ACTIN FILAMENTS
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
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CC
DR EMBL: U48938; AAB03696.1; -
DR EMBL: AF102173; AAC72407.1; -
DR EMBL: AL162459; CAB88325.1; -
DR PDB: 1F7S; 1S-NOV-00.
DR InterPro: IPR002108; Actbind_cofln.
DR Pfam: PF00241; cofilin_ADF.1.
DR ProDom: PD002129; Actbind_cofln; 1.
DR SMART: SM00102; ADF.1.
DR PROSITE: PS00325; ACTIN_DEPOLYMERIZING; 1.
KW Actin-binding; Multigene family; 3D-structure.
FT DOMAIN 92 111 ACTIN-BINDING (POTENTIAL).
FT SEQUENCE 139 AA; 16112 MW; E9429E0F23A944F CRC64;
SO
Query Match 14.7%; Score 108; DB 1; Length 139;
Best Local Similarity 27.7%; Pred. No. 0.0035;
Matches 31; Conservative 26; Mismatches 53; Indels 2; Gaps 2;
OY 17 KLRFRFRKETDMAAIIMKVDKROMVYLEEPEQ-NIS-PEELKMELEPQRPQVYVSYKY 75
DB 15 KLRLEELKAKTRHPIYKIEKQYVVEGPIQIYTFEFAACLPADDECRVAIYDPDF 74
OY 76 VHDGKVSYPICFTSSPGVCKPEQOMTAGSKNRLVQTAELTVFEIRPTD 127
DB 75 VTAENCKSKRIFFIAMCPDIAKVASKMILYASSKDRFRRELDGIV-ELQATD 125
RESULT 7

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ID	ADP3_ARATH	STANDARD:	PRT:	139 AA.
AC	Q9ZSK3: Q9ZUE7;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Actin-depolymerizing factor 4 (ADP-4) (AtADP4).			
CN	ADP4 OR AT5G59890 OR MN10.13.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	Eurosids II; Brassicales; Brassicaceae; Arabidopsids.			
OX	NCBI_TaxID:3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RX	MEDLINE=21307188; PubMed=11414611;			
RT	Dong C.-H., Kost B., Xia G., Chua N.-H.;			
RT	"Molecular identification and characterization of the Arabidopsis			
RT	AtADP1, AtADP5 and AtADP6 genes."			
RL	Plant Mol. Biol. 45:517-527 (2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RX	MEDLINE=99087489; PubMed=9872454;			
RT	Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,			
RT	Tabata S.;			
RT	"Structural analysis of Arabidopsis thaliana chromosome 5. VII.			
RT	Sequence features of the regions of 1,013,767 bp covered by sixteen			
RT	physically assigned pl and TAC clones."			
RL	DNA Res. 5:297-308(1998).			
CC	-1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENTS			
CC	(F-ACTIN) AND BINDS TO ACTIN MONOMERS (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADP FAMILY.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF102822; AAD09110.1; -			
DR	EMBL; AB015475; BAB08357.1; -			
DR	HSSP; Q39250; 1E7S.			
DR	InterPro; IPR002108; Actbind_coflin.			
DR	Pfam; PF00241; coflin_ADP.1.			
DR	ProDom; PD002129; Actbind_coflin; 1.			
DR	SMART; SM00102; ADP.1.			
DR	PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.			
RW	Actin-binding; Multigene family.			
FT	DOMAIN 92 111 ACTIN-BINDING (POTENTIAL).			
FT	CONFLICT 117 117 I -> R (IN REF. 1).			
FT	CONFLICT 134 134 L -> W (IN REF. 1).			
SO	SEQUENCE 139 AA; 16034 MW; 57F95F55/F42P863 CRC64;			
Query Match	14.3%; Score 105; DB 1; Length 139;			
Best Local Similarity	25.0%; Pred. No. 0.0066;			
Matches	28; Conservative 30; Mismatches 52; Indels 2; Gaps 2;			
QY	17 KLRFRFRKETDMAIIMKVDKRDQNVVLEEFQNT-SPEELKMLPERQPRFVVS YK 75			
DB	15 KLRFLLEAKRTHRFPIYVRIEKQKVIVERKGEPIILTYEDFASLPADECRVAYLPD 74			
QY	76 VHDGSRVSYPLCFITFSFVPGCKPRQDQMYAASKNRNVLTATLTKVFEIRTD 127			
DB	75 VTAENCKSKSTFTLAWCPDVAKVSKMISKDKRFKRELDGIQV-ELQARD 125			

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AC 09ZSK4: 28-FEB-2003 (Rel. 41, Created)
AD 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Actin-depolymerizing factor 3 (ADF 3) (AtADF3).
GN ADF3 OR AT5G59880 OR MN10.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosipis II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21307188; PubMed=11414611.
RA Dong C.-H., Kost B., Xia G., Chua N.-H.,
RT Molecular identification and characterization of the Arabidopsis
RT AtADF1, AtADF5 and AtADF6 genes."
RL Plant Mol. Biol. 45:517-527 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=99087489; PubMed=9872454;
RA Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VII.
RT Sequence features of the regions of 1,013,767 bp covered by sixteen
RT physically assigned P1 and TAC clones."
RL DNA Res. 5:297-308 (1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT S5P consortium (Salk/Stanford/PGEc)."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERALS ACTIN FILAMENTS
CC (F-ACTIN) AND BINDS TO ACTIN MONOMERS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
CC -----
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CC -----
CC DR EMBL; AF102821; AAD09109.1; -
CC DR EMBL; AB015475; BAB08356.1; -
CC DR EMBL; AF360169; AAK25879.1; -
CC HSSP; Q39250; 1P7S.
CC InterPro; IPR002108; Actbind_cofin.
CC Pfam; PF00241; cofillin_ADF.1.
CC ProDom; PD002129; Actbind_cofin; 1.
CC SMART; SM00102; ADF.1.
CC PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
KW Actin-binding; Multigene family.
FT DOMAIN 92 111 ACTIN-BINDING (POTENTIAL).
FT SEQUENCE 139 AA; 15922 MW; D3325AAV7IDDD0102E CRC64;
SQ
Query Match 14.1%; Score 104; DB 1; Length 139;
Best Local Similarity 24.1%; Pred. No. 0.0081;
Matches 27; Conservative 33; Mismatches 50; Indels 2; Gaps 2;
QY 17 KLRFRPRKKTDNAIIWKYDKRQMVVLEEFQ-NISPEELKMLPERQPRVVSXKY 75
DB 15 KLRKEMELKTRKTRHRIIYKIELOKOYIVKIGEPGQTHEDLASLPADRCRYAIFDPEF 74
QY 76 VHDGGRSYPLCLFIFFSSVYGCKPRQDQMMYAGSKRRLVOTALTIVFEKRTD 127
DB 75 VSSGCVPRSRIRFFVAMSPDARVBSKMIYAKRFRKRELDGIVQ-ELQAVD 125

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RESULT 9
ADFL_PETHY STANDARD: PRT: 139 AA.
AC Q9FV12;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
GN Actin-depolymerizing factor 1 (ADF 1).
OS ADF1.
OC Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20534787; PubMed=11080583;
RA Mun J.-H., Yu H.-J., Lee H.S., Kwon Y.M., Lee J.S., Lee I., Kim S.-G.;
RT "Two closely related cDNAs encoding actin-depolymerizing factors of
  Petunia are mainly expressed in vegetative tissues."
RL Gene 257:167-176(2000).
CC -1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERES ACTIN FILAMENTS
  (F-ACTIN) AND BINDS TO ACTIN MONOMERS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF183903; AAG16973.1; -
DR HSSP; Q39250; 1F7S.
DR InterPro; IPR002108; Actbind_cofin.
DR Pfam; PF00241; cofillin_ADF; 1.
DR PRODOM; PD002129; Actbind_cofin; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
KW Actin-binding; Multigene family.
FT DOMAIN 92 111 ACTIN-BINDING (POTENTIAL).
FT SEQUENCE 139 AA; 16041 MW; 008073E2C6A28F0B CRC64;
SQ
Query Match 14.0%; Score 103; DB 1; Length 139;
Best Local Similarity 25.9%; Pred. No. 0.01;
Matches 29; Conservative 28; Mismatches 53; Indels 2; Gaps 2;
QY 17 KLRFRFRKKTNDNAIIMKVDKQRMVLEEEFQ-NISPELKMELPERQPRFVVSXY 75
DB 15 KLRFLKAKRTHRFYIKIEKQYVVERIGEPESYEDFASLPEDECRVAVYDFE 74
QY 76 VHDGGRSYPLCFIFSSPGVCKPEQOMMYAGSKNRVLQVTAELTVFELRTTD 127
DB 75 VTAENCKSKRIEFLAMCPDPAVRARSKMIYASSKDRFRRELDGIY-ELQACD 125

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RP SEQUENCE FROM N.A.
RX MEDLINE=20534787; PubMed=11080583;
RA Mun J.-H., Yu H.-J., Lee H.S., Kwon Y.M., Lee J.S., Lee I., Kim S.-G.;
RT "Two closely related cDNAs encoding actin-depolymerizing factors of
  Petunia are mainly expressed in vegetative tissues."
RL Gene 257:167-176(2000).
CC -1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERES ACTIN FILAMENTS
  (F-ACTIN) AND BINDS TO ACTIN MONOMERS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
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CC -----
DR EMBL; AF183904; AAG16974.1; -
DR HSSP; Q39250; 1F7S.
DR InterPro; IPR002108; Actbind_cofin.
DR Pfam; PF00241; cofillin_ADF; 1.
DR PRINTS; PR00006; COFILIN.
DR PRODOM; PD002129; Actbind_cofin; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
KW Actin-binding; Multigene family.
FT DOMAIN 92 111 ACTIN-BINDING (POTENTIAL).
FT SEQUENCE 143 AA; 16510 MW; 408E035D0E61C05C CRC64;
SQ
Query Match 13.7%; Score 100.5; DB 1; Length 143;
Best Local Similarity 28.4%; Pred. No. 0.017;
Matches 33; Conservative 26; Mismatches 46; Indels 11; Gaps 4;
QY 13 ELTEKLKFRFRKKTNDNAIIMKVDKQRMVLEEEFQ-NISPELKMELPERQPRFVVSXY 71
DB 20 ELKAK-RYRPF-----IIKIEKQYVVERIGEPESYEDFTAGLPADCRVAVY 70
QY 72 SYRVVHDGGRSYPLCFIFSSPGVCKPEQOMMYAGSKNRVLQVTAELTVFELRTTD 127
DB 71 DFDPMTEKNINCKSKRIEFLAMCPDPAVRARSKMIYASSKDRFRRELDGIY-ELQACD 125

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RESULT 11
ACTP_ACACA STANDARD: PRT: 137 AA.
AC P37167;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE Actophorin.
OS Acanthamoeba castellanii (Acanthamoeba).
OC Eukaryota; Acanthamoebidae; Acanthamoeba.
OX NCBI_TaxID=5755;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 1-105, AND X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=93363583; PubMed=8357799;
RA Oulrik S., Maciver S.K., Ampe C., Doberstein S.K., Katsner D.A.,
  van Damme J., Vandekerckhove J., Pollard T.D.;
RT "Primary structure of and studies on Acanthamoeba actophorin."
RL Biochemistry 32:8525-8533(1993).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=97290450; PubMed=9145107;
RA Leonard S.A., Gittis A.G., Petrella E.C., Pollard T.D., Latman E.E.;
RT "Crystal structure of the actin-binding protein actophorin from
  Acanthamoeba."
RL Natl. Struct. Biol. 4:369-373(1997).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS).
RX MEDLINE=98411306; PubMed=9737968;
RA Blanchonin L., Pollard T.D.;
RT "Interaction of actin monomers with Acanthamoeba actophorin"

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RT (ADF/cofilin) and profilin."
RL J. Biol. Chem. 273:25106-25111(1998).
CC -1- FUNCTION: FORMS A ONE TO ONE COMPLEX WITH MONOMERIC ACTIN. CAN
CC REGULATE THE POOL AVAILABLE FOR POLYMERIZATION. SEVERS ACTIN
CC FILAMENTS IN A DOSE-DEPENDENT MANNER.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M9361; AAA02909.1; -.
CC PDB: 1AHQ; 04-SEP-97.
CC InterPro: IPR002108; Actbind_cofiln.
CC Pfam: PF00241; cofilin_ADF. 1.
CC PRINTS: PR00006; COFILIN.
CC PRODOM: PD002129; Actbind_cofiln. 1.
CC SMART: SM00102; ADF. 1.
CC PROSITE: PS00325; ACTIN_DEPOLYMERIZING. 1.
CC Actin-binding; 3D-structure.
CC INIT MET 0 0
CC MOD_RES 1 1 BLOCKED.
CC DOMAIN 86 105 ACTIN-BINDING (POTENTIAL).
CC STRAND 4 5
CC HELIX 7 19
CC STRAND 24 29
CC TURN 31 32
CC STRAND 35 41
CC TURN 44 45
CC HELIX 48 52
CC TURN 53 54
CC STRAND 57 58
CC TURN 61 71
CC STRAND 72 73
CC TURN 74 84
CC STRAND 87 88
CC TURN 91 107
CC HELIX 109 110
CC STRAND 113 117
CC TURN 120 123
CC HELIX 125 132
CC TURN 133 133
CC SEQUENCE 137 AA; 15422 MW; D16030AB4EF6347B CRC64;

Query Match 13.3%; Score 97.5; DB 1; Length 137;
Best Local Similarity 25.7%; Pred. No. 0.031;
Matches 28; Conservative 30; Mismatches 46; Indels 5; Gaps 4;

QY 32 IMKVDKROMVLEE-EFQNSPELKMELPERQPRFVYVYKYVHDGRSYDLCEFF 90
DB 25 VFFKMASTVEVVEVVEGPNATYEDFSQDLPERCRAIFYEYQVGGGRN-KITFIL 83
QY 91 SSPVCCPEQOMMYAGSKNRNLVOTAELEKVFERTTD--DLTEAWLOEK 137
DB 84 WAPDSAPIKSKMMYTSTKDSIKKLVGIQV-EVQATDAEISEDAVSEK 131

RESULT 12
ADP2_ARATH STANDARD; PRT; 137 AA.
AC Q39251; O9LZT2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Actin-depolymerizing factor 2 (ADF-2) (AtADF2).
GN ADF2 OR AT3G46000 OR F16L2_210.

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OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Staiger C.J., Ashworth S.L.;
RT "Actin depolymerizing factor from Arabidopsis thaliana severs
RT polymers and binds to monomers in a pH-dependent manner."
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseid M.,
RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaler B.,
RA Delseny M., Boutry M., Griveil L.A., Maché R., Puldomenech P.,
RA De Simone V., Choise N., Artiguenave F., Robert C., Brotier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurdach E., Drzonek H., Erile H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Scharfe M., Schoen O., Barques M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Liauro C., Purnelle B., Masy D.,
RA de Haan M., Maistre A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Uterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Millscher J., Sellers P., Gill J.E., Feldlyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shilipo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana."
RL Nature 408:820-822(2000).
CC -1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENTS
CC (F-ACTIN) AND BINDS TO ACTIN MONOMERS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
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CC -----
CC EMBL: U48939; AAB03697.1; -.
CC DR EMBL: AL162459; CAB82824.1; ALT_INIT.
CC DR HSSP: Q39250; 1F7S.
CC DR InterPro: IPR002108; Actbind_cofiln.
CC DR Pfam: PF00241; cofilin_ADF. 1.
CC DR PRODOM: PD002129; Actbind_cofiln. 1.
CC DR SMART: SM00102; ADF. 1.
CC DR PROSITE: PS00325; ACTIN_DEPOLYMERIZING. 1.
CC Actin-binding; Multigene family.
CC DOMAIN 90 109 ACTIN-BINDING (POTENTIAL).
CC SEQUENCE 137 AA; 15745 MW; BE2852817394046 CRC64;

Query Match 12.9%; Score 95; DB 1; Length 137;
Best Local Similarity 25.2%; Pred. No. 0.053;
Matches 28; Conservative 26; Mismatches 55; Indels 2; Gaps 2;

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CC BIND G- AND F-ACTIN IN A 1:1 RATIO OF COFILIN TO ACTIN. IT IS THE
CC MAJOR COMPONENT OF INTRANUCLEAR AND CYTOPLASMIC ACTIN RODS
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTRANUCLEAR AND CYTOPLASMIC
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
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CC -----
CC EMBL: D89939; BA114039.1; -.
CC EMBL: Z98600; CAB11258.1; -.
CC PIR: T43245; T43245.
CC HSSP: Q03048; ICOF.
CC GenedB, Spombe: SPAC20G4.06c; -.
CC InterPro: IPR002108; Actbind_cofln.
CC Pfam: PF00241; cofilin_ADF; 1.
CC PRINTS: PR00006; COFILIN.
CC ProDom: PD002129; Actbind_cofln; 1.
CC SMART: SM00102; ADF; 1.
CC PROSITE: PS00325; ACTIN-DEPOLYMERIZING; 1.
CC Actin-binding; Cytoskeleton.
CC FT DOMAIN 88 107 ACTIN-BINDING (POTENTIAL).
CC SEQUENCE 137 AA; 15620 MW; ECC6D354C959E04 CRC64;

Query Match
Best Local Similarity 12.6%; Score 92.5; DB 1; Length 137;
Matches 26; Conservative 33; Mismatches 50; Indels 13; Gaps 3;

QY 9 EVDPELTLEKLRFRKEDNNAIIMKYDKDQWVLEEFQNISPEELKMLPEROPRF 68
DB 7 KVSPECLAFQELKLGKSL--RYVYFKMNDKTELVEKSKSDKDFDLDPKDCRY 64
QY 69 VVYSKRYVHDGRVSYPLCFIFSSPVGCKPEQOMKAYGSKNRL-----VQTAELT 118
DB 65 AIYDFEFLMGEG-VANKIIFISWSPVAPIRKSKWYSSKDTLRRAPFTGIGTDIQTDFS 123
QY 119 KV 120
DB 124 EV 125

RESULT 15
COFI_DICDI
ID COFI_DICDI STANDARD; PRT; 137 AA.
AC P54706;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cofilin.
GN (COFA OR COFI) AND (COFB OR COF2).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxId=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX2;
RX MEDLINE=95256267; PubMed=7738034;
RA Aizawa H., Sutoh K., Tsubuki S., Kawashima S., Ishii A., Yahara I.,
RT "Identification, characterization, and intracellular distribution of
RT cofilin in Dictyostelium discoideum.",
RL J. Biol. Chem. 270:10923-10932(1995).
CC -1- FUNCTION: CONTROLS REVERSIBLY ACTIN POLYMERIZATION AND
CC DEPOLYMERIZATION IN A PH-SENSITIVE MANNER. IT HAS THE ABILITY TO
CC BIND G- AND F-ACTIN IN A 1:1 RATIO OF COFILIN TO ACTIN. IT IS THE
CC MAJOR COMPONENT OF INTRANUCLEAR AND CYTOPLASMIC ACTIN RODS
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTRANUCLEAR AND CYTOPLASMIC

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CC (BY SIMILARITY).
CC -1- MISCELLANEOUS: THERE ARE TWO GENES FOR COFILIN IN D.DISCOIDEUM,
CC THEY ENCODE FOR IDENTICAL PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
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CC -----
CC EMBL: D37980; BA07198.1; -.
CC EMBL: D37981; BA07199.1; -.
CC HSSP: Q03048; ICOF.
CC SWISS-2DPAGE: P54706; DICTY.
CC DICTYDB: DD01059; COFA.
CC DICTYDB: DD01059; COFB.
CC InterPro: IPR002108; Actbind_cofln.
CC Pfam: PF00241; cofilin_ADF; 1.
CC PRINTS: PR00006; COFILIN.
CC ProDom: PD002129; Actbind_cofln; 1.
CC SMART: SM00102; ADF; 1.
CC PROSITE: PS00325; ACTIN-DEPOLYMERIZING; 1.
CC Nuclear protein; Actin-binding; Cytoskeleton; Multigene family.
CC SEQUENCE 137 AA; 15224 MW; 0C0B057354F46F3 CRC64;

```

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Query Match
Best Local Similarity 12.4%; Score 91.5; DB 1; Length 137;
Matches 29; Conservative 26; Mismatches 49; Indels 5; Gaps 4;

```

```

QY 32 IIMKYDKDQWVLEEF-QNISPEELKMLPEROPRFVVSRYKYVHDGRVSYPLCFIF 90
DB 27 IYRISDSKELIVDSTLPAGCSFDEFKCLPENECRYVLDYQ-KEEGAQSKKICFA 85
QY 91 SSPVCKPEQOMMYGSKNRLVQTAELKVEIRFTD--DLTEALQK 137
DB 86 WCPDTANIKRMMATSSKDSLRKACVGIQV-ELQGTDASEVNDSCFYER 133

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Search completed: September 23, 2003, 15:09:18
Job time : 25 secs

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OM protein - protein search, using sw model

Run on: September 23, 2003, 15:05:44 : Search time 98 Seconds
(without alignments)
373.913 Million cell updates/sec

Title: US-10-004-832-2

Perfect score: 735

Sequence: 1 MSDSLVCEVDPDELTEKLRK.....IRTTDDLTEAMLOEKLSFRR 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_23:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	722	98.2	142	4	Q8TD26
2	695	94.6	142	11	Q9ERL7
3	622	84.6	154	4	Q9BS35
4	619	84.2	142	11	Q9ERL8
5	617	83.9	142	11	Q9COR3
6	600	81.6	142	13	Q9IBG6
7	379.5	51.6	138	5	Q9VJL6
8	373	50.7	138	5	Q9VJL6
9	261	35.5	145	5	Q17247
10	185	25.2	65	5	Q8MAA5
11	175	23.8	141	3	Q13808
12	123.5	16.3	328	3	Q94399
13	119.5	16.3	333	5	Q20173
14	116.5	15.9	149	3	Q21256
15	113	15.4	252	4	Q8BCD3
16	113	15.4	350	4	Q12792

17	111.5	15.2	133	10	Q65277	065277 arabidopsis
18	111.5	15.2	140	10	Q8LC13	08LC13 arabidopsis
19	111	15.1	347	11	Q8BN77	08BN77 mus musculus
20	111	15.1	349	11	Q920P5	Q920P5 mus musculus
21	110	15.0	143	10	Q8SAG3	Q8SAG3 vitis vinif
22	110	15.0	347	11	Q9DCR8	Q9DCR8 mus musculus
23	109.5	14.9	343	5	Q9VEM9	Q9VEM9 drosophila
24	109	14.8	349	4	Q9Y3P5	Q9Y3P5 homo sapien
25	107	14.6	138	10	Q9XEN2	Q9XEN2 populus x c
26	106	14.4	129	10	Q9SW69	Q9SW69 malus domes
27	105	14.3	132	10	Q94A13	Q94A13 arabidopsis
28	104.5	14.2	156	6	Q8MIK3	Q8MIK3 bos taurus
29	104	14.1	145	10	Q8H9D5	Q8H9D5 solanum tub
30	103.5	14.1	133	3	Q9L2P3	Q9L2P3 arabidopsis
31	102.5	13.9	138	5	Q8T1J2	Q8T1J2 dictyosteli
32	102.5	13.9	140	10	Q9M5Y4	Q9M5Y4 elaeis guin
33	102.5	13.9	145	10	Q9AYV6	Q9AYV6 oryza sativ
34	100.5	13.7	130	10	Q65603	Q65603 arabidopsis
35	99	13.5	153	10	Q9FWC0	Q9FWC0 oryza sativ
36	98.5	13.4	350	11	Q91YR1	Q91YR1 mus musculus
37	98.5	13.4	350	11	Q09132	Q09132 mus musculus
38	97.5	13.3	142	10	Q43655	Q43655 tritium ae
39	96	13.1	139	10	Q8H2P8	Q8H2P8 oryza sativ
40	95.5	13.0	130	10	Q49606	Q49606 arabidopsis
41	95	12.9	146	10	Q8LCM6	Q8LCM6 arabidopsis
42	93.5	12.7	137	10	Q8H2B7	Q8H2B7 nicotiana t
43	92.5	12.6	130	10	Q9FHC4	Q9FHC4 arabidopsis
44	92.5	12.6	137	10	Q8LFB6	Q8LFB6 arabidopsis
45	91.5	12.4	137	10	Q8H2B6	Q8H2B6 nicotiana t

ALIGNMENTS

RESULT 1
Q8TD26 PRELIMINARY: PRT: 142 AA.
ID Q8TD26
AC Q8TD26:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Gila maturation factor gamma.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Asai K., Kawai Y., Inoue Y., Ueki T., Yamamoto M., Miura Y., Kato T.;
RT "Homo sapiens Gila Maturation Factor gamma (GMFG) genomic DNA.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040440; BAB86591.1; -
DR InterPro: IPR002108; Actbind_cofin.
DR Pfam: PF00241; cofilin_ADF.1.
DR SMART: SM00102; ADF.1.
SQ SEQUENCE 142 AA; 16859 MW; DB64BD80B8BCDD5A CRC64;

Query Match 98.2%; Score 722; DB 4; Length 142;
Best Local Similarity 98.6%; Pred. No. 9.5e-63;
Matches 140; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	MSDSL	VCEVDPDELTEKLRKFRFKETDNAAIIMKVDKRDQMVYLEEFQNI	SPELKME	60
Db	1	MSDSL	VCEVDPDELTEKLRKFRFKETDNAAIIMKVDKRDQMVYLEEFQISPELKME		60
QY	61	LPERP	PRVVSYSKYVHDDGRVSYPLCTFSSPVCKREQQMYAGSNRRVQTAELTKV		120
Db	61	LPERP	PRVVSYSKYVHDDGRVSYPLCTFSSPVCKREQQMYAGSNRRVQTAELTKV		120
QY	121	FEIRTT	DDLTTEAMLOEKLSFRR		142
Db	121	FEIRTT	DDLTTEAMLOEKLSFRR		142

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RESULT 2
O9ERL7 PRELIMINARY; PRT; 142 AA.
ID O9ERL7;
AC O9ERL7;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Gila maturation factor-gamma (0610039G16Rik protein) (2310057N07R1k
DE protein) (Gila maturation factor, gamma).
GN GMEG OR 0610039G16R1K OR 2310057N07R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss/TOPS OF1; TISSUE=Liver;
RC Bourgeois F., Guilmet F., Levacher B., Mas C., Simonneau M.J.;
RT "Identification and full-length cloning of GMEB, a putative
RT intracellular kinase regulator, expressed in proliferating
RT telencephalon stem cells."
RT Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo, Kidney, and Tongue;
RC MEDLINE=21085660; PubMed=11217851;
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojocori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Flischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirni L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi T.,
RA Guncic S., Hill D., Hoffmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombert P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wells C., Whitaker C., Wilmink L.,
RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (Jul-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF297221; AAC22804.1; -
DR EMBL: AK014214; BAB29210.1; -
DR EMBL: AK002834; BAB2392.1; -
DR EMBL: AK009967; BAB2617.1; -
DR EMBL: BC011468; AAH11488.1; -
DR MGD: MGI:1927133; Gmfg.
DR InterPro: IPR002108; Actbind_cofin.
DR Pfam: PF00241; cofillin_ADF.1.
DR SMART: SM00102; ADF.1.
SO SEQUENCE 142 AA; 16748 MW; 25367F2B949378710 CRC64;

Query Match 94.6%; Score 695; DB 11; Length 142;
Best Local Similarity 93.7%; Pred. No. 4,le-60;
Matches 133; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
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Oy 1 MSDSLVCEVDPETELKRFKRETNDNAIIMKVKDRQMVVLEEFONISPEELKME 60
Db 1 MSDSLVCEVDPETELKRFKRETNDNAIIMKVKDRQMVVLEEFONISPEELKME 60
Oy 61 LPERQPRVYVSYKYVHDDGVSYPICFIFSSPVGCKPEQOMMYAGSKNRLVQAEITKV 120
Db 61 LPERQPRVYVSYKYVHDDGVSYPICFIFSSPVGCKPEQOMMYAGSKNRLVQAEITKV 120

RESULT 3
O9BS35 PRELIMINARY; PRT; 154 AA.
ID O9BS35;
AC O9BS35;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Gila maturation factor, beta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bladder;
RC Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: BC005359; AAH05359.1; -
DR InterPro: IPR002108; Actbind_cofin.
DR Pfam: PF00241; cofillin_ADF.1.
DR SMART: SM00102; ADF.1.
SO SEQUENCE 154 AA; 18110 MW; 712DB64F30E530FD CRC64;

Query Match 84.6%; Score 622; DB 4; Length 154;
Best Local Similarity 82.3%; Pred. No. 5,9e-53;
Matches 116; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

Oy 1 MSDSLVCEVDPETELKRFKRETNDNAIIMKVKDRQMVVLEEFONISPEELKME 60
Db 1 MSELVACDAVEDLVEKLRFRFRKRTNNAIIMKIDKRVVLDELSIDELKDE 60
Oy 61 LPERQPRVYVSYKYVHDDGVSYPICFIFSSPVGCKPEQOMMYAGSKNRLVQAEITKV 120
Db 61 LPERQPRVYVSYKYVHDDGVSYPICFIFSSPVGCKPEQOMMYAGSKNRLVQAEITKV 120

Oy 121 FEIRTTDLTEAWLQEKLSFF 141
Db 121 FEIRTTDLTEAWLREKLGFF 141

RESULT 4
O9ERL8 PRELIMINARY; PRT; 142 AA.
ID O9ERL8;
AC O9ERL8;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Gila maturation factor-beta.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss/TOPS OF1; TISSUE=Telencephalon;
RC Bourgeois F., Guilmet F., Mas C., Bulfone A., Levacher B.,
RA Moalic J.M., Simonneau M.;
RT "Identification and isolation of a full-length clone of mouse GMEB
RT (Gmfb), a putative intracellular kinase regulator, differentially
RT expressed in telencephalon.";
RT CytoGenet. Cell Genet. 92:304-309(2001).
DR EMBL: AF297220; AAC22803.1; -
DR MGD: MGI:1927133; Gmfb.
DR InterPro: IPR002108; Actbind_cofin.
DR Pfam: PF00241; cofillin_ADF.1.
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OS Drosophila melanogaster (fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 ON NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mkios G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.M., Benos P.V., Berman B.P., Brodsky J., Brottler P.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dudin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbagyan C.,
 RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
 RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Pacle J.M.,
 RA Palazolo M., Plittman G.S., Pan S., Pollard J., Puri V., Shen M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shee H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Wolley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Bazon J., An H., Baldwin D., Bazon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galie R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibbagyan C., Jatali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nuno J.,
 RA Pacle J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirska R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of Drosophila melanogaster genome.";
 RL submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC Miera S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hirdbeck P., Huang Y., Kaminler J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;

RT "Annotation of Drosophila melanogaster genome.";
 RL submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC FlyBase;
 RA Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Berkeley;
 RX MEDLINE=99403001; PubMed=10471707;
 RA Ashburner M., Miera S., Roote J., Lewis S.E., Blazey R., Davis T.,
 RA Doyle C., Galie R., George R., Harris N., Hartzell G., Harvey D.,
 RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
 RA Palazolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitehead K.,
 RA Celniker S., Rubin G.M.;
 RT "An exploration of the sequence of a 2.9-Mb region of the genome of
 Drosophila melanogaster: the Adh region.";
 RL Genetics 153:179-219(1999).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Berkeley;
 RA Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazey R.G.,
 RA Butenoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
 RA Farfan D.E., Galie R., George R.A., Harris N.L., Hoskins R.A.,
 RA Houston K.A., Hummasti S.R., Karra K., Keane L., Kim E., Lee B.,
 RA Lewis S., Li P., Lomolan M.A., Mazda P., Moshrefi A., Moshrefi M.,
 RA Nixon K., Pacle J.M., Park S., Pfeiffer B., Poon L., Sequelra A.,
 RA Sechi H., Snir E., Svirska R.R., Wan K.H., Weinburg T., Zhang R.,
 RA Zieran L.L., Rubin G.M.;
 RL submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AE003650; AAF53517.2;
 DR EMBL; AE003415; AAF4499.1;
 DR FlyBase; FBgn0028894; BG:DS02740.9.
 DR InterPro; IPR002108; Actbind_cofin.
 DR Pfam; PF00241; cofilin_ADF.1.
 DR SMART; SM00102; ADF.1
 SO SEQUENCE 138 AA; 16451 MW; F7B07868054BC31 CRC64;
 Query Match 51.6%; Score 379.5; DB:5; Length 138;
 Best Local Similarity 52.2%; Pred. No. 2.3e-29;
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 AC Q17247;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Gila maturation factor BmGF.
 GN BmGF.
 OS Brugia malayi.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 CC Onchoercidae; Brugia.
 ON NCBI_TaxID=6279;
 RN [1]

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 23, 2003, 15:08:53 ; Search time 30 Seconds

(Without alignments)
200.271 Million cell updates/sec

Title: US-10-004-832-2

Perfect score: 735
Sequence: 1 MSDSLVCEVDPPELTKLRK.....IRTTDDLEAMLOEKISFR 142

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: Issued Patents_AA:
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3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/PCtUS.COMB.pep:*
7: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	735	100.0	142	2	US-08-187-186A-2
2	735	100.0	142	2	US-08-442-497C-2
3	735	100.0	142	4	US-09-333-033-2
4	735	100.0	142	5	PCT-US94-05186-2
5	723	98.4	142	4	US-09-663-600A-229
6	622	84.6	141	4	US-09-333-033-9
7	618	84.1	141	2	US-08-187-186A-5
8	614	83.5	141	2	US-08-442-497C-9
9	558	75.9	109	4	US-09-663-600A-213
10	513	15.4	350	1	US-08-184-252A-2
11	513	15.4	350	2	US-09-123-851-3
12	513	15.4	350	2	US-08-728-520-3
13	513	15.4	350	5	PCT-US95-00601-2
14	513	15.4	357	2	US-09-123-851-4
15	513	15.4	357	2	US-08-728-520-4
16	513	15.4	357	2	US-09-123-851-1
17	513	15.4	343	2	US-08-728-520-1
18	513	15.4	496	4	US-09-107-532A-1164
19	513	15.4	308	4	US-09-134-001C-4400
20	513	15.4	1678	4	US-09-535-008-69
21	513	15.4	1678	4	US-09-535-008-65
22	513	15.4	1681	4	US-09-535-008-77
23	513	15.4	1682	4	US-09-535-008-73
24	513	15.4	1686	4	US-09-107-532A-5118
25	513	15.4	1646	4	US-09-535-008-67
26	513	15.4	1647	4	US-09-535-008-2
27	513	15.4	1649	4	US-09-535-008-75

28	71	9.7	1650	4	US-09-535-008-71	Sequence 71, Appl
29	69	9.4	254	3	US-09-318-448-25	Sequence 25, Appl
30	69	9.4	428	4	US-09-134-001C-2942	Sequence 2942, Ap
31	69	9.4	793	4	US-09-107-532A-5141	Sequence 5141, Ap
32	68.5	9.3	433	4	US-09-595-424-2	Sequence 2, Appl
33	68.5	9.3	494	4	US-09-595-424-4	Sequence 4, Appl
34	68.5	9.3	658	4	US-09-595-424-6	Sequence 6, Appl
35	68	9.3	454	3	US-08-764-870-5	Sequence 5, Appl
36	68	9.3	454	3	US-08-980-115-5	Sequence 5, Appl
37	68	9.3	454	6	5260432-2	Sequence 4479, Ap
38	68	9.3	783	6	5231168-2	Sequence 5876, Ap
39	67.5	9.2	887	4	US-09-328-352-4479	Sequence 4479, Ap
40	67.5	9.2	1151	4	US-09-328-352-5876	Sequence 5876, Ap
41	67	9.1	1169	4	US-09-255-828-20	Sequence 20, Appl
42	66.5	9.0	251	4	US-09-286-981B-4	Sequence 4, Appl
43	66.5	9.0	307	4	US-09-075-460-16	Sequence 16, Appl
44	66.5	9.0	414	4	US-09-286-981B-10	Sequence 10, Appl
45	66.5	9.0	564	3	US-09-308-022-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-187-186A-2
Sequence 2, Application US/08187186A
Patent No. 5922572
GENERAL INFORMATION:
APPLICANT: Craig A. Rosen; Henrik Olsen;
APPLICANT: Mark D. Adams; and Ewen Kirkness
TITLE OF INVENTION: HAEMOPOIETIC MATURATION FACTOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08187,186A
FILING DATE: January 25, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-46 (PF105)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-187-186A-2

Query Match 100.0%; Score 735; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 2, 5e-83;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSDSLVCEVDPPELTKLRFRFRKRDNAALIMKVKDKRQMVYLEEFQNISPELTKME 60
|||||
Db 1 MSDSLVCEVDPPELTKLRFRFRKRDNAALIMKVKDKRQMVYLEEFQNISPELTKME 60

QY 61 LPERQPRFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120
|||||
Db 61 LPERQPRFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120
QY 121 FEIRTTDDLTEAMLOEKLSFPR 142
|||||
Db 121 FEIRTTDDLTEAMLOEKLSFPR 142

RESULT 2

US-08-442-497C-2
Sequence 2, Application US/08442497C
Patent No. 5986069
GENERAL INFORMATION:
APPLICANT: KIRKNESS, ET AL.
TITLE OF INVENTION: Human Haemopoietic Maturation
TITLE OF INVENTION: Factor
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,497C
FILING DATE: Concurrently
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,186
FILING DATE: 25 JAN 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05186
FILING DATE: 10 MAY 1994
ATTORNEY/AGENT INFORMATION:
NAME: MULHINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-282 (PF105P1)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-442-497C-2

Query Match 100.0%; Score 735; DB 2; Length 142;

Best Local Similarity 100.0%; Pred. No. 2, 5e-83;

Matches 142: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDSLVCEVDPPELTERKFRFRKETDMAIIMKVDKROMVYLEEFONISPEELKME 60
|||||
Db 1 MSDSLVCEVDPPELTERKFRFRKETDMAIIMKVDKROMVYLEEFONISPEELKME 60
QY 61 LPERQPRFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120
|||||
Db 61 LPERQPRFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120
QY 121 FEIRTTDDLTEAMLOEKLSFPR 142
|||||
Db 121 FEIRTTDDLTEAMLOEKLSFPR 142

RESULT 3
US-09-333-033-2
Sequence 2, Application US/09333033
Patent No. 6346246
GENERAL INFORMATION:
APPLICANT: Kirkness et al.
TITLE OF INVENTION: Human Haemopoietic Maturation Factor
FILE REFERENCE: PF105P1D1
CURRENT APPLICATION NUMBER: US/09/333,033
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 08/442,497
PRIOR FILING DATE: 1995-05-16
PRIOR APPLICATION NUMBER: 08/187,186
PRIOR FILING DATE: 1994-01-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 142
TYPE: PRT
ORGANISM: Homo sapiens
US-09-333-033-2

Query Match 100.0%; Score 735; DB 4; Length 142;
Best Local Similarity 100.0%; Pred. No. 2, 5e-83;
Matches 142: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDSLVCEVDPPELTERKFRFRKETDMAIIMKVDKROMVYLEEFONISPEELKME 60
|||||
Db 1 MSDSLVCEVDPPELTERKFRFRKETDMAIIMKVDKROMVYLEEFONISPEELKME 60
QY 61 LPERQPRFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120
|||||
Db 61 LPERQPRFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120
QY 121 FEIRTTDDLTEAMLOEKLSFPR 142
|||||
Db 121 FEIRTTDDLTEAMLOEKLSFPR 142

RESULT 4

PCT-US94-05186-2
Sequence 2, Application PC/TUS9405186
GENERAL INFORMATION:
APPLICANT: KIRKNESS, ET AL.
TITLE OF INVENTION: Haemopoietic Maturation Factor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05186
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,186
FILING DATE: 25 JANUARY 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-46
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700


```

; REFERENCE/DOCKET NUMBER: 325800-46 (PF105)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-187-186A-5

Query Match      84.1%; Score 618; DB 2; Length 141;
Best Local Similarity 82.3%; Pred. No. 7.8e-69;
Matches 116; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

QY 1 MSDSLVYCEVDPELTETKRFKRFKRETDNNAIIMKVKDRQMVYLEEFGNISPELME 60
   |||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MSELVYCDVADVEDLVETKRFKRFKRETNNAIIMKIDKRLVYLDEKEGISPELDE 60

QY 61 LPERQPRFVYSYKYVHDDGVSYPLCFIFSSPYGCKPEQOMYAGSKNRLVQTAEITKV 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LPERQPRFVYSYKYVHDDGVSYPLCFIFSSPYGCKPEQOMYAGSKNKLVTAEITKV 120

QY 121 FEIRTTDLTFEAWLOEKLSFF 141
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 FEIRTTDLTFEAWLREKLGFF 141

RESULT 8
US-08-442-497C-9
; Sequence 9, Application US/08442497C
; Patent No. 5986069
; GENERAL INFORMATION:
; APPLICANT: KIRKNESS, ET AL.
; TITLE OF INVENTION: Human Haemopoietic Maturation
; TITLE OF INVENTION: Factor
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESS: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,497C
; FILING DATE: Concurrently
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/187,186
; FILING DATE: 25 JAN 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05186
; FILING DATE: 10 MAY 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-282 (PF105P1)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1744
; TELEFAX: 201-994-1700
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 AMINO ACIDS
; TYPE: AMINO ACID
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; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-442-497C-9

Query Match      83.5%; Score 614; DB 2; Length 141;
Best Local Similarity 81.6%; Pred. No. 2.4e-68;
Matches 115; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSDSLVYCEVDPELTETKRFKRFKRETDNNAIIMKVKDRQMVYLEEFGNISPELME 60
   |||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MSELVYCDVADVEDLVETKRFKRFKRETNNAIIMKIDKRLVYLDEKEGISPELDE 60

QY 61 LPERQPRFVYSYKYVHDDGVSYPLCFIFSSPYGCKPEQOMYAGSKNRLVQTAEITKV 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LPERQPRFVYSYKYVHDDGVSYPLCFIFSSPYGCKPEQOMYAGSKNKLVTAEITKV 120

QY 121 FEIRTTDLTFEAWLOEKLSFF 141
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 FEIRTTDLTFEAWLREKLGFF 141

RESULT 9
US-09-663-600A-213
; Sequence 213, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouquelert, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 213
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-663-600A-213

Query Match      75.9%; Score 558; DB 4; Length 109;
Best Local Similarity 98.2%; Pred. No. 1.5e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 34 MKVVKDRQMVYLEEFGNISPELMEKELPERQPRFVYSYKYVHDDGVSYPLCFIFSSP 93
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MKVVKDRQMVYLEEFGNISPELMEKELPERQPRFVYSYKYVHDDGVSYPLCFIFSSP 60

QY 94 VGCKPEQOMYAGSKNRLVQTAEITKVFEIRTTDLTFEAWLOEKLSFFR 142
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 VGCKPEQOMYAGSKNRLVQTAEITKVFEIRTTDLTFEAWLOEKLSFFR 109

RESULT 10
US-08-184-252A-2
; Sequence 2, Application US/08184252A
; Patent No. 5573935
```



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GENERAL INFORMATION:
APPLICANT: Beeler, John F.
APPLICANT: Larocheville, William
APPLICANT: Aaronson, Stuart A.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE A6
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/184,252A
FILING DATE: 18-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelien, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH084.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-184-252A-2

Query Match      15.4%, Score 113; DB 1; Length 350;
Best Local Similarity 26.4%; Pred. No. 1.2e-05;
Matches 38; Conservative 33; Mismatches 53; Indels 20; Gaps 7,

QY      6 VCCVYDELTETKLRFRKRTDNNAIIMKVDKDRQVYLEEFQNIISPEELKMLPERQ 65
DB      178 VAFDISEAFALKEKLNNRQ---VYOLEIDINKEIIL---ANTNTEIK-DLPRRI 229
QY      66 P-----RVVYSYKRVHDDGRVSYDLCFFESP-VGCKREDDQMYAGSKNRIVQTAE---- 116
DB      230 PKDSARKHFFELYKSH-EGDYLEISIVFLYSMPGYTCSIRERWLYSSCKSLLEIVEROLQ 288
QY      117 --LTKVFETRTDLDLTFEAWLOEKL 138
DB      289 MDVIRKIEIDNGDELTFADFLTEEV 312

RESULT 11
US-09-123-851-3
; Sequence 3, Application US/09123851
; Patent No. 5958405
; GENERAL INFORMATION:
; APPLICANT: Goll, Surya K.
; TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

```

```

SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,851
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/728,520
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0136 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 451482
US-09-123-851-3

Query Match 15.4%; Score 113; DB 2; Length 350;
Best Local Similarity 26.4%; Pred.No.1,2e-05;
Matches 38; Conservative 33; Mismatches 53; Indels 20; Gaps 7

QY 6 VCCVDEPLETEKLRFRFRKETDNNAIIMKYDKDROMVYLEEFONISPELIKMLPERQ 65
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 178 VAFPISEAEAFQALEKLNRRQLN---YVQLEIDIKNEIIL---ANTNTEIK-DLPKRI 229

QY 66 P----REVVYSYKRVHVDGRVSYPLCFIESSP-VGCKREQQMAYGSKNRIVQTAE---- 116
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 230 PKDSARAHFELFKHSH-EGDYLESIVFLYSMPGYTCSIRERMLYSSCKRLLEIVERQLQ 288
   : : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 117 -LTKVFEIRTPDDELTEAMLOEKL 138
   : : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 289 MDVIRKTEIDNGDELTADELVEEV 312
   : : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 12
US-08-728-520-3
: Sequence 3, Application US/08728520
: Patent No. 5994112
: GENERAL INFORMATION:
: APPLICANT: GOLL, Surya K.
: TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: U.S.
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 1.5
: CURRENT APPLICATION DATA:
: FILING DATE: Filed Herewith
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0136 US

```

```

1      RESULT 13
2      PCT-US95-00601-2
3      : Sequence 2, Application PC/TUS9500601
4      : GENERAL INFORMATION:
5      : APPLICANT: United States of America Department of Health and Human
6      : SERVICES
7      : APPLICANT: Services
8      : TITLE OF INVENTION: PROTEIN TYROSINE KINASE A6
9      : NUMBER OF SEQUENCES: 8
10     : CORRESPONDENCE ADDRESS:
11     : ADDRESSEE: Knobbe, Martens Olson & Bear
12     : STREET: 620 Newport Center Drive, Sixteenth Floor
13     : CITY: Newport Beach
14     : STATE: CA
15     : COUNTRY: USA
16     : ZIP: 92660
17     : COMPUTER READABLE FORM:
18     : MEDIUM TYPE: Floppy disk
19     : COMPUTER: IBM PC compatible
20     : OPERATING SYSTEM: PC-DOS/MS-DOS
21     : SOFTWARE: PatentIn Release #1.0, Version #1.25
22     : CURRENT APPLICATION DATA:
23     : APPLICATION NUMBER: PCT/US95/00601
24     : FILING DATE:
25     : CLASSIFICATION:
26     : ATTORNEY/AGENT INFORMATION:
27     : NAME: Israelson, Ned A.
28     : REGISTRATION NUMBER: 29,655
29     : REFERENCE/DOCKET NUMBER: N10084,001A
30     : TELECOMMUNICATION INFORMATION:
31     : TELEPHONE: (619) 235-8550
32     : TELEFAX: (619) 235-0176
33     : INFORMATION FOR SEQ. ID NO. 2:
34     : SEQUENCE CHARACTERISTICS:
35     : LENGTH: 350 amino acids
36     : TYPE: amino acid
37     : TOPOLOGY: linear
38     : MOLECULE TYPE: protein
39     : PCT-US95-00601-2
40
41     Query Match          15.4%; Score 113; DB 5; Length 350;
42     Best Local Similarity 26.4%; Pred. No. 1,2e-05;

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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123.851
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/728.520
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0136 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1166579
US-09-123-851-4

Query Match          14.5%, Score 106.5; DB 2; Length 357;
Best Local Similarity 22.8%; Pred. Misat: 0.5;
Matches 37; Conservative 30; Mismatches 60; Indels 35; Gaps 5

QY      6 VCCEDEPLTEKLRFRFKETDNAAITMKYDKOKOMVYLEEPONISPEELKMLPERQ 65
       1 11 : 11 : : 11 : : 11 : : 11 : : 11 : : 11 :
Db      171 VAFPDRAVEAEALRLASQ---LSFYOLSVDTLNEAIKLTGTLSEPSQLASKVPBDK
       1 11 : 11 : : 11 : : 11 : : 11 : : 11 : : 11 :
QY      66 PRFVVYSKYVHDDGRVSYPLCFIRSP-VGCKPPOOMMYAGSKRNLVQTAE----- 116
       11 : 11 : : 11 : : 11 : : 11 : : 11 : : 11 :
Db      228 PRIFYFNNDHW-EKVPOOCTLFILTSLPSSGSSIKERKLVSCKRPFLSAMONOYGVIIT 286
       11 : 11 : : 11 : : 11 : : 11 : : 11 : : 11 :
QY      117 -----LTKVEEIR-----TTDDLTEAMLOE 136

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Db 287 NKFLQKRSNKKMKIRKIFLKRKNDMEVDARDLSEKALLE 328

RESULT 15

US-08-728-520-4

; Sequence 4, Application US/08728520

; Patent No. 5994112

GENERAL INFORMATION:

; APPLICANT: GOLI, Surya K.

; TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/728,520

; FILING DATE: Filed Herewith

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0136 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-845-4166

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 357 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 116579

; US-08-728-520-4

Query Match 14.5%; Score 106.5; DB 2; Length 357;

Best Local Similarity 22.8%; Pred No. 7.6e-05;

Matches 37; Conservative 30; Mismatches 60; Indels 35; Gaps 5;

Qy 6 VVCEVDPLETKLRFRFRKEDNAIIMKYDKDQWVLLSEEFQNTSPSELKMLPERQ 65
Db 171 VAFPYDRNAEELRLQASQ---LSFVQLSVDTLNEAIKLGTLSEPSQLASKVPRDK 227
Qy 66 PRFVYISKYVHDGSRVYPLCFIFSSP-VGCKPEQOMYAGSKNRIVQTAE----- 116
Db 228 PRYTFYNPDHW-EGVPOQCTLFYISLPSGSSIKERMLYSSCKGPFLSAQNOYGVYT 286
Qy 117 -----LTKVFEIR-----TTDDLTEAWLOE 136
Db 287 NKFLQKRSNKKMKIRKIFLKRKNDMEVDARDLSEKALLE 328

Search completed: September 23, 2003, 15:13:01
Job time : 31 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 23, 2003, 15:07:23 : Search time 27 Seconds

(without alignments)
783.069 Million cell updates/sec

Title: US-10-004-832-2

Perfect score: 735

Sequence: 1 MSDSLVCEVDPPELTLEKLRK.....IRTTDDLTFAWLQEKLSFPR 142

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 556269 seqs, 148893369 residues

Total number of hits satisfying chosen parameters: 556269

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PC1_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PC1US_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	735	100.0	142	14	US-10-004-832-2
2	723	98.4	142	12	US-10-319-763-229
3	699	95.1	147	9	US-09-925-302-642
4	614	83.5	141	14	US-10-004-832-9
5	558	75.9	109	12	US-10-319-763-213
6	113	15.4	350	11	US-09-251-225-3
7	113	15.4	350	15	US-10-087-340-266
8	113	15.4	350	15	US-10-205-823-241
9	113	15.4	385	9	US-09-925-299-966
10	113	15.4	385	11	US-09-925-299-966
11	113	15.4	385	15	US-10-106-698-4598
12	109.5	14.9	224	14	US-10-108-605-277
13	108	14.7	348	10	US-09-969-384-19
14	106.5	14.5	357	11	US-09-251-225-4
15	103	14.0	343	11	US-09-251-225-1

16	78.5	10.7	166	15	US-10-205-342-21	Sequence 21, Appl
17	78.5	10.7	166	15	US-10-205-823-72	Sequence 72, Appl
18	74.5	10.1	487	11	US-09-298-523B-66	Sequence 66, Appl
19	71.5	9.7	722	15	US-10-029-495-5	Sequence 5, Appl
20	71	9.7	1647	11	US-09-824-574-4	Sequence 4, Appl
21	70.5	9.6	299	9	US-09-815-242-10563	Sequence 10563, A
22	70.5	9.6	487	11	US-09-298-523B-9	Sequence 9, Appl
23	69.5	9.5	685	9	US-09-801-574-6	Sequence 6, Appl
24	69	9.4	310	10	US-09-925-300-1602	Sequence 1602, Ap
25	68.5	9.3	189	11	US-09-764-891-3897	Sequence 3897, Ap
26	68.5	9.3	454	9	US-09-764-881-148	Sequence 148, App
27	68	9.3	454	9	US-09-797-727-2	Sequence 2, Appl
28	68	9.3	454	11	US-09-814-604-3	Sequence 3, Appl
29	67.5	9.2	148	14	US-10-108-605-27	Sequence 27, Appl
30	67.5	9.2	911	15	US-10-204-887-123	Sequence 123, App
31	67	9.1	440	11	US-09-910-186A-8	Sequence 8, Appl
32	67	9.1	1169	12	US-10-241-596-20	Sequence 20, Appl
33	67	9.1	1713	15	US-10-270-333-177	Sequence 177, App
34	66.5	9.0	168	9	US-09-945-301-5	Sequence 5, Appl
35	66.5	9.0	251	12	US-10-254-995-4	Sequence 4, Appl
36	66.5	9.0	254	11	US-09-056-019-9	Sequence 9, Appl
37	66.5	9.0	307	12	US-10-216-667-16	Sequence 16, Appl
38	66.5	9.0	326	9	US-09-841-132-585	Sequence 585, App
39	66.5	9.0	376	11	US-09-056-019-7	Sequence 7, Appl
40	66.5	9.0	413	11	US-09-056-019-35	Sequence 35, Appl
41	66.5	9.0	414	12	US-10-254-995-10	Sequence 10, Appl
42	66.5	9.0	481	11	US-09-298-523B-6	Sequence 6, Appl
43	66.5	9.0	483	11	US-09-298-523B-10	Sequence 10, Appl
44	66.5	9.0	539	11	US-09-298-523B-54	Sequence 54, Appl
45	66.5	9.0	581	11	US-09-298-523B-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1	
US-10-004-832-2	
Sequence 2, Application US/10004832	
Publication No. US20020146408A1	
GENERAL INFORMATION:	
APPLICANT: Kirkness et al.	
TITLE OF INVENTION: Human Haemopoietic Maturation Factor	
FILE REFERENCE: PF105PID2	
CURRENT APPLICATION NUMBER: US/10/004,832	
CURRENT FILING DATE: 2001-12-07	
PRIOR APPLICATION NUMBER: US 09/333,033	
PRIOR FILING DATE: 1999-06-15	
PRIOR APPLICATION NUMBER: US 08/442,497	
PRIOR FILING DATE: 1995-05-16	
PRIOR APPLICATION NUMBER: US 08/187,186	
PRIOR FILING DATE: 1994-01-25	
NUMBER OF SEQ ID NOS: 9	
SOFTWARE: PatentIn version 3.1	
SEQ ID NO 2	
LENGTH: 142	
TYPE: PRT	
ORGANISM: Homo sapiens	
US-10-004-832-2	
Query Match	100.0%; Score 735; DB 14; Length 142;
Best Local Similarity	100.0%; Pred. No. 5.1e-75;
Matches 142; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MSDSLVCEVDPPELTLEKLRKFRFKETDAAITMKVVDKRDQVYLEEEOISPEELKME 60
DB	1 MSDSLVCEVDPPELTLEKLRKFRFKETDAAITMKVVDKRDQVYLEEEOISPEELKME 60
QY	1 LPEROPRVVYSYKVVHDGRVSYPLCFEFPSCCKPEQOMVAGSKNRVLQPTAELIKV 120
DB	1 LPEROPRVVYSYKVVHDGRVSYPLCFEFPSCCKPEQOMVAGSKNRVLQPTAELIKV 120
QY	121 FEIRTTDDLTFAWLQEKLSFPR 142
DB	121 FEIRTTDDLTFAWLQEKLSFPR 142

Db 121 FEIRTTDDLTEAMLQEKLSFFR 142

RESULT 2

US-10-319-763-229

Sequence 229, Application US/10319763

Publication No. US20030144490A1

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean-Baptiste

APPLICANT: Duclert, Aymeric

APPLICANT: Bougueleret, Lydie

TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS

FILE REFERENCE: G-031.US04.DIV

CURRENT FILING DATE: US/10/319,763

PRIOR FILING DATE: 2002-12-10

PRIOR APPLICATION NUMBER: 60/066,677

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/069,957

PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/074,121

PRIOR FILING DATE: 1998-02-09

PRIOR APPLICATION NUMBER: 60/081,563

PRIOR FILING DATE: 1998-04-13

PRIOR APPLICATION NUMBER: 60/096,116

PRIOR FILING DATE: 1998-08-10

PRIOR APPLICATION NUMBER: 60/099,273

PRIOR FILING DATE: 1998-09-04

NUMBER OF SEQ ID NOS: 229

SOFTWARE: Patent.pm

SEQ ID NO 229

LENGTH: 142

TYPE: PRT

ORGANISM: Homo sapiens

US-10-319-763-229

Query Match

Best Local Similarity 98.4%; Score 723; DB 12; Length 142;

Matches 140; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MSDSLVYCEVDPPELTKRFRFRKEDTNNAIIMKVKDRQMVVLEEFONISPEELKME 60

1 MSDSLVYCEVDPPELTKRFRFRKEDTNNAIIMKVKDRQMVVLEEFONISPEELKME 60

Db 1 MSDSLVYCEVDPPELTKRFRFRKEDTNNAIIMKVKDRQMVVLEEFONISPEELKME 60

1 MSDSLVYCEVDPPELTKRFRFRKEDTNNAIIMKVKDRQMVVLEEFONISPEELKME 60

QY 61 LPERQPRFVYVYKYYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120

61 LPERQPRFVYVYKYYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120

Db 61 LPERQPRFVYVYKYYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120

61 LPERQPRFVYVYKYYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120

QY 121 FEIRTTDDLTEAMLQEKLSFFR 142

121 FEIRTTDDLTEAMLQEKLSFFR 142

Db 121 FEIRTTDDLTEAMLQEKLSFFR 142

121 FEIRTTDDLTEAMLQEKLSFFR 142

RESULT 3

US-09-925-302-642

Sequence 642, Application US/09925302

Patent No. US20020044941A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA104

CURRENT APPLICATION NUMBER: US/09/925,302

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05918

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 896

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 642

LENGTH: 147

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (2)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (103)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-302-642

Query Match

Best Local Similarity 95.1%; Score 699; DB 9; Length 147;

Matches 135; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 VCEVDPPELTKRFRFRKEDTNNAIIMKVKDRQMVVLEEFONISPEELKMELEPERQ 66

7 VCEVDPPELTKRFRFRKEDTNNAIIMKVKDRQMVVLEEFONISPEELKMELEPERQ 66

Db 12 VCEVDPPELTKRFRFRKEDTNNAIIMKVKDRQMVVLEEFONISPEELKMELEPERQ 71

12 VCEVDPPELTKRFRFRKEDTNNAIIMKVKDRQMVVLEEFONISPEELKMELEPERQ 71

QY 67 RFVYVSYKYYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKVFEIRTT 126

67 RFVYVSYKYYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKVFEIRTT 126

Db 72 RFVYVSYKYYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKVFEIRTT 131

72 RFVYVSYKYYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKVFEIRTT 131

QY 127 DDLTEAMLQEKLSFFR 142

127 DDLTEAMLQEKLSFFR 142

Db 132 DDLTEAMLQEKLSFFR 147

132 DDLTEAMLQEKLSFFR 147

RESULT 4

US-10-004-832-9

Sequence 9, Application US/10004832

Publication No. US20020146408A1

GENERAL INFORMATION:

APPLICANT: Kirkness et al.

TITLE OF INVENTION: Human Haemopoietic Maturation Factor

FILE REFERENCE: PF105P1D2

CURRENT APPLICATION NUMBER: US/10/004,832

PRIOR FILING DATE: 2001-12-07

PRIOR APPLICATION NUMBER: US 09/333,033

PRIOR FILING DATE: 1999-06-15

PRIOR APPLICATION NUMBER: US 08/442,497

PRIOR FILING DATE: 1995-05-16

PRIOR APPLICATION NUMBER: US 08/187,186

PRIOR FILING DATE: 1994-01-25

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.1

SEQ ID NO 9

LENGTH: 141

TYPE: PRT

ORGANISM: Homo sapiens

US-10-004-832-9

Query Match

Best Local Similarity 83.5%; Score 614; DB 14; Length 141;

Matches 115; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSDSLVYCEVDPPELTKRFRFRKEDTNNAIIMKVKDRQMVVLEEFONISPEELKME 60

1 MSDSLVYCEVDPPELTKRFRFRKEDTNNAIIMKVKDRQMVVLEEFONISPEELKME 60

Db 1 MSELVYCDVAEDVELEKTRFRFRKEDTNNAIIMKVKDRQMVVLEEFONISPEELKME 60

1 MSELVYCDVAEDVELEKTRFRFRKEDTNNAIIMKVKDRQMVVLEEFONISPEELKME 60

QY 61 LPERQPRFVYVYKYYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120

61 LPERQPRFVYVYKYYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120

Db 61 LPERQPRFVYVYKYYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120

61 LPERQPRFVYVYKYYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120

QY 121 FEIRTTDDLTEAMLQEKLSFFR 141

121 FEIRTTDDLTEAMLQEKLSFFR 141

Db 121 FEIRTTDDLTEAMLQEKLSFFR 141

121 FEIRTTDDLTEAMLQEKLSFFR 141

RESULT 5

US-10-319-763-213

Sequence 213, Application US/10319763

Publication No. US20030144490A1

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean-Baptiste

APPLICANT: Duclert, Aymeric

```

LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 451482
US-09-251-225-3

Query Match      15.4%; Score 113; DB 11; Length 350;
Best Local Similarity 26.4%; Pred. No. 0.00021;
Matches 38; Conservative 33; Mismatches 53; Indels 20; Gaps 7;

QY      6 VVCEVDPELTETKLRKFRFRKFTDNNAIIMKYDKDRQMYLLEEFONISPEELKNEPQQ 65
Db      178 VAFISIRAEAFQALEKRLNNRQLN---VQLEIDIKNEIIL----ANTTFEIK-DLPKR 229
QY      66 P-----RFVVSYYKRVHODGRVSYPLCFEFSSP-VGCKREQOMYAGSNRLVQNAE----- 116
Db      230 PKDSARVYFFELTKHSH-EGDYLESTIVFTYSPGYTCSIRERMLYSSCKSLLEIVERQLQ 288
QY      117 -LTFKVEFIRTTDDLTEAMLOEKL 138
Db      289 MDVIRKIEIDNGDELTDLFYEEV 312

RESULT 7
US-10-097-340-266
Sequence 266, Application US/10097340
Publication No. US20030087250A1
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOERSCHE
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERSEY
APPLICANT: Michael MORRISEY
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
APPLICANT: Peter VEIBY
APPLICANT: Gordon B. MILLS
APPLICANT: Robert C. BAST, Jr.
APPLICANT: Karen LU
APPLICANT: Rosemarie SCHMANDT
APPLICANT: Xumei ZHAO
APPLICANT: Karen GLATT
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIORITY APPLICATION NUMBER: 60/276,025
PRIORITY FILING DATE: 2001-03-14
PRIORITY APPLICATION NUMBER: 60/325,149
PRIORITY FILING DATE: 2001-09-26
PRIORITY APPLICATION NUMBER: 60/276,026
PRIORITY FILING DATE: 2001-03-14
PRIORITY APPLICATION NUMBER: 60/324,967
PRIORITY FILING DATE: 2001/09/26
PRIORITY APPLICATION NUMBER: 60/311,732
PRIORITY FILING DATE: 2001-08-10
PRIORITY APPLICATION NUMBER: 60/325,102
PRIORITY FILING DATE: 2001-09-26
PRIORITY APPLICATION NUMBER: 60/323,580
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 266
LENGTH: 350
TYPE: PRT
ORGANISM: Homo sapiens

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: CURRENT APPLICATION NUMBER: US/10/108,605
 : CURRENT FILING DATE: 2002-03-27

: PRIORITY NUMBER: 60/176,418
 : PRIOR APPLICATION NUMBER: US 60/176,418
 : PRIOR FILING DATE: 2000-01-14

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; SEQ ID NO 277
;
; LENGTH: 224

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US-10-108-605-277

Best Local similarity 29.9%; Pred. no. 0.00029;
Matches 32; Conservative 24; Mismatches 36; Indels 15; Gaps 5;

Db 88 IEEQIHVSRAKVELADLPKQVPEDHARHYHLEFRTHEDGYEESY--VFVYSMPGYS C 145

[illegible]

RESULT 13
US-09-969-384-19
Sequence 10 Amplification: 16/00060394

```

; GENERAL INFORMATION:
; APPLICANT: Moore, et al.
; FIRM OR INVENTOR: Hughes Case Development, Inc. and Hughes

```

; CURRENT APPLICATION NUMBER: US/09/969,384
 ; CURRENT FILING DATE: 2001-10-03
 ; PUBLICATION NUMBER: US 2001/00513

; PRIOR APPLICATION NUMBER: 60/236,384
 ; PRIOR FILING DATE: 2000-09-29

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; NUMBER OF SEQ ID NOS: 27
;
; SOFTWARE: PatentIn Ver. 2.0

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ORGANISM: Homo sapiens

Query Match	14.7%;	Score 108;	DB 10;	Length 348;
Best Local Similarity	26.4%;	Pred. No. 0.00078;		

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QY      10 VDPETLETKRFRFRKTDNAALIMKYDKDRQWVLEEFQNISPEELKMEIPEQP--- 66
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67 -REVVYSKYVHDDGRVSYPLCFIFSSP-VGCKPEQOMMYAGSKNRLVQTA-----ELT 118

QY 119 KVF E I R T D D L T E A W L Q E K L 138
| | | : | | : | : : :
| | | : | | : | : : :

RESULT 14

```

; Publication No. US20030099652A1
;
; sequence 4, Application US/09231423
;
GENERAL INFORMATION:

```

APPLICANT: GOLI, SURYA K.
TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/251,225
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0136 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1166579
US-09-251-225-4

Query Match 14.5%; Score 106.5; DB 11; Length 357;
Best Local Similarity 22.8%; Pred. No. 0.0012;
Matches 37; Conservative 30; Mismatches 60; Indels 35; Gaps 5;

QY 6 VCCEVDPELTLEKRRFRKRETDNAALIMKYDKDROMVLEEEFQNISPEELKMLPEPQ 65
DB 171 VAFVDRNAEALQLASQK---LSFVQLSVDTLNEAIKLEGTLESLEPSQLASKVPRDK 227
QY 66 PRFVVSXKYVHDDGRVSYPLCFITFSSP-VGCKPEQOMYAGSKNRLVQTA----- 116
DB 228 PRYTFYNEDHTW-EGVPOQCTLFITYSLPSSGSSIKERMLYSSCKGPFLSAONQYGVYT 286
QY 117 -----LTKEFEIR-----TTDDLTEAMLOE 136
DB 287 NKEPLQKRSNKMFKIREKIFELKRLKNDMEVDARDLSEKALLE 328

RESULT 15
US-09-251-225-1
Sequence 1, Application US/09251225
Publication No. US20030099652A1
GENERAL INFORMATION:
APPLICANT: GOLI, SURYA K.
TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/251,225
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0136 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
US-09-251-225-1

Query Match 14.0%; Score 103; DB 11; Length 343;
Best Local Similarity 26.4%; Pred. No. 0.0028;
Matches 37; Conservative 32; Mismatches 51; Indels 20; Gaps 7;

QY 10 VDPETLEKRRFRKRETDNAALIMKYDKDROMVLEEEFQNISPEELKMLPEPQ--- 66
DB 182 LQPERQRLQDL---KQNMVYIQMKLDLERETI---ELVHTPTDV-AQLPRVVRDA 233
QY 67 -RFVVSXKYVHDDGRVSYPLCFITFSSP-VGCKPEQOMYAGSKNRLVQTA-----ELT 118
DB 234 ARYHXPFLYKINH-EGDPLESVVFLYSMPGYKCSIKERMLYSSCKSRLLDSVEQDFHLEIA 292
QY 119 KVEFIRTTDLTEAMLOEKL 138
DB 293 KKEIGQAEELTAELFYDEV 312

Search completed: September 23, 2003, 15:12:24
Job time : 28 secs